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Result
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Perfect score:
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Listing first 45 summaries
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 ,
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T42011
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GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS

Query Match
Best Local Similarity
Matches 298; Conserv

Conservative

100.0%; Score 1543; DB 1; 100.0%; Pred. No. 7.3e-129; tive 0; Mismatches 0;

Length

298; 0

Gaps

0

| RESULT 1  S03894  ADP,ATP carrier protein T3 - human N;Alternate names: ADP,ATP carrier protein T2 (misidentification); mitochondrial ADP, C;Species: Homo sapiens (man) C;Date: 17-Mar-2000 #sequence revision 17-Mar-2000 #text_change 17-Mar-2000 C;Accession: S03894; B28116 R;Cozens, A.L.; Runswick, M.J.; Walker, J.E. J. Mol. Biol. 206, 261-260, 1989 A;Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP A;Reference number: S03893; MUID:89236396 A;Reference number: S03893; MUID:89236396 A;Residues: not compared with conceptual translation A;Molecule type: DNA A;Residues: not compared with conceptual translation A;Reference number: A94197; MUID:89236396 R;Houldsworth, J.; Attardi, G. A;Reference number: M94197; MUID:8924845 A;Reference number: M94197; MUID:88124845 A;Reference number: M94197; MUID:88124845 A;Accession: B28116 A;Molecule type: mRNA A;Residues: 36-104, R.,106, A,109-298 <houd- 36-104,="" <houd-="" a,109-298="" a;ac<="" a;accession:="" a;cross-references:="" a;experimental="" a;molecule="" a;references:="" a;residues:="" b28116="" b28125="" c;genetics:="" gb:j03592;="" liver="" mrna="" nid:9339722;="" pid:9339723="" pidn:aaa36750.1;="" r.,106,="" source:="" th="" type:=""><th>ALIGNMENTS</th><th>30 743 48.2 379 2 T04608 ADP, ATP carrier pr<br/>31 742 48.1 385 1 S29852 ADP, ATP carrier pr<br/>32 742 48.1 382 2 S33630 ADP, ATP carrier pr<br/>33 739.5 47.8 309 2 A24849 ADP, ATP carrier pr<br/>34 737.5 47.8 309 2 A24849 ADP, ATP carrier pr<br/>35 734.5 44.2 298 2 T24023<br/>36 681.5 44.2 298 2 T24023<br/>37 520.5 33.7 327 2 T51577 ADP, ATP carrier pr<br/>39 381 24.8 325 2 T04273 ADP, ATP carrier pr<br/>40 372 24.1 358 2 T45934 ADP, ATP carrier pr<br/>41 370.5 23.9 381 2 T45934 ADP, ATP carrier pr<br/>42 369.5 23.9 381 2 T45934 hypothetical prote<br/>43 368 23.8 475 2 T50686<br/>44 363 23.8 475 2 T50686 Paroxisomal Cardep<br/>45 344.5 22.3 332 2 T47703</th></houd-> | ALIGNMENTS | 30 743 48.2 379 2 T04608 ADP, ATP carrier pr<br>31 742 48.1 385 1 S29852 ADP, ATP carrier pr<br>32 742 48.1 382 2 S33630 ADP, ATP carrier pr<br>33 739.5 47.8 309 2 A24849 ADP, ATP carrier pr<br>34 737.5 47.8 309 2 A24849 ADP, ATP carrier pr<br>35 734.5 44.2 298 2 T24023<br>36 681.5 44.2 298 2 T24023<br>37 520.5 33.7 327 2 T51577 ADP, ATP carrier pr<br>39 381 24.8 325 2 T04273 ADP, ATP carrier pr<br>40 372 24.1 358 2 T45934 ADP, ATP carrier pr<br>41 370.5 23.9 381 2 T45934 ADP, ATP carrier pr<br>42 369.5 23.9 381 2 T45934 hypothetical prote<br>43 368 23.8 475 2 T50686<br>44 363 23.8 475 2 T50686 Paroxisomal Cardep<br>45 344.5 22.3 332 2 T47703 |
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R; Battini, R.; Ferrari, S.; Kaczmarek, L.; J. Biol. Chem. 262, 4355-4359, 1987 A; Title: Molecular cloning of a cDNA for a A; Reference number: A29132; MUID:87166056 A; Accession: A29132
                                                                                                                                                                                                                    ADP,ATP carrier protein T2 - human
N;Alternate names: mitochondrial ADP,ATP translocase
C;Species: Homo sapiens (man)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Powell, S.J.; Medd, S.M.; Runswick, M.J.;
Blochemistry 28, 866-873, 1989
A;Title: Two bovine genes for mitochondrial
A;Reference number: A43646; MUID:89229093
A;Accession: B43646
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A;Cross-references:
R;H@uldsworth, J.;
                                     A; Molecule type: mRNA
A; Residues: 1-298 <BAT>
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C;Accession: A29132; C28116
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A; Residues: 1-298 < POW>
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C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999
C;Accession: B43646
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Eest Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60
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J.; Attardi,
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GB:J02683;
Attardi, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.0%;
97.7%;
                NID:g179246; PIDN:AAA35579.1;
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Pred. No. 4e-126;
4; Mismatches
                                                                                                               human ADP/ATP carrier which is growth-regula
                                                                                                                                                           Calabretta,
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A,Map position: Xd13-Xd26
A;Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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A; Nolecule type: mRNA
A; Residues: 47-65,'G',67-110,'L',112-161,'G',163-298 <HOU>
A; Cross-references: GB:J03591; NID:g339720; PIDN:AAA36749.1;
A; Cross-references: Clone pHAT3
                                                                                                                                                                                                                                                                                         R;Shinohara, Y.; Kamida, M.; Yamazaki, N.;
Biochim. Biophys. Acta 1152, 192-196, 1993
A;Title: Isolation and characterization of
A;Reference number: I60173; MUID:94002161
                                                                                                                                                                                                                                                                                                                                                                                     adenine nucleotide translocator - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
C;Accession: I60173
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A;Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level
A;Reference number: A94197; MUID:88124845
A;Accession: C28116
                                                                                                                    A; Introns: 37/3;
                                                                                                                                           A;Gene: anti
                                                                                                                                                                                    A;Cross-references: EMBL:X61667; NID:g400426; PIDN:CAA43842.1; PID:g400427
                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-298 < RES>
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                                                                                                                    200/1; 247/1
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                                                                                                                                                                                                                                                     from
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                                                                                                                                                                                                                                                                                                                       cDNA clones
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                             <ACP2>
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Query Match
Best Local Similarity
Matches 267; Conser

Conservative

18;

Mismatches

92.3**%**; 89.6**%**;

Score 1424; Pred. No. 2.

DB 2; .4e-118; les 13;

Length 298;

0

Gaps

0;

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N;Alternate names: ADP/APP transcern.

C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Species: 14-Nov-1983 #sequence_revision 22-Jul-1994 #text_change 22-.
C;Accession: A43646; A24822; A03181; A61343; S69369
R;Powell, S.J; Medd, S.M.; Runswick, M.J.; Walker, J.E.
Blochemistry 28, 866-873, 1989
A;Title: Two bovine genes for mitochondrial ADP/ATP translocase exp
A;Reference number: A43646; MUID:89229093
A;Accession: A43646
A;Molecule type: mRNA
A;Residues: 1-298 <POW>
A;Residues: 1-298 <POW>
A;Residues: GB:M24102; NID:9529414; PIDN:AAA30768.1; PID:9
Ry Rasmussen, U.B.; Wohlrab, H.

Blochem. Biophys. Res. Commun. 138, 850-857, 1986
A; Fittle: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinal App/ATP-carrier: two distinal Approximation and two distinal Approximation: A24822

A; Molecule type: mRNA
A; Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1; PID.
A; Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1; PID.
A; Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1; PID.
A; Cross-reference and acid sequence of the ADP/ATP carrier from A; Residues: 2-51, X', 53-70, 'X', 72-109, 'X', 111-298 <AQU>
A; Accession: A03181; MUID:82188267

A; Molecule type: protein A; Reference number: A61343; MUID:82046808

A; Molecule type: protein A; Residues: 205-298 <BAB>
A; Molecule type: protein A; Residues: 205-298 <BAB>
A; Molecule type: protein A; Reference number: S69369; MUID:82046808

A; Residues: 205-298 <BAB>
A; Molecule type: protein A; Reference number: S69369; MUID:82046808

A; Residues: 49-63;154-168 <Cpr>
A; Molecule type: protein A; Reference number: S69369; MUID:95172058

A; Molecule type: protein A; Reference number: S69369; MUID:95172058

A; Molecule type: protein A; Reference number: S69369; MUID:95172058

A; Molecule type: protein A; Muid: Sequence determination of the cytosol and transportant the inner mitochondrial membrane C; Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein is synthesized in the cytosolic ADP and manual protein is approximated in the cytosolic ADP and manual protein is approximated in the cytosolic ADP and manual protein is approximated in the cytosolic ADP and manual protein is approximated in the cytosolic ADP and manual protein is approximated in the cytosolic ADP
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ADP, ATP carrier protein T1 - mouse

N:Alternate names: adenine nucleotide car

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06

C:Accession: S37210

R:Laplace, C.: Costet, P.

submitted to the EMBL Data Library, Septe

A:Reference number: S37210

A:Accession: S37210
                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-298 < LAP>
A; Residues: 1-298 < LAP>
A; Cross-references: EMBL: X74510; NID: 9402627; PIDN: CAA52616.1; PIC: Genetics:
A; Gene: ANC1
C; Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein IC; Superfamily: ADP, ATP carrier protein Protein IC; Superfamily: ADP, ATP carrier protein repeat homology <ACP1>
F; 110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>
F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Keywords: acetylated amino end; duplication; homodimer; methylated F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>F;2/Modified site: acetylated amino end (Ser) (in mature form) #statu F;52/Modified site: N6-methyllysine (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
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Best Local
                                                                                                                                                                                                                                               Matches
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les 266; Conservative
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                                                                                                                                                                                      MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
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                                        GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
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QSGRKGADIMYTGTVDCWRKIAKDEGPKAFFKGAWSNVLRGMGGAFVLVLYDEIKKFV
                                                                                 IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120
                                                                                                                                                                  MGDQALSFLKDFLAGGIAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
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                                                                                                                                                                                                                                               265;
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                                                                                                                                                                                                                                                                   91.9%;
88.9%;
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89.3%;
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Pred. No. 3
                                                                                                                                                                                                                                                                   Score 1418; DB 2;
Pred. No. 8.1e-118;
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les 13;
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C:Keywords: duplication; homodimer; mitochongriou, cumumants (C:Keywords: duplication; homodimer; mitochongriou, cumumants (C:Keywords: duplication; homodimer; mitochongriou, cumumants (F;2-298/Product: ADP,ATP carrier protein repeat homology <ACP1>F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP2>F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP3>F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 4q35-4q35
C; Superfamily: ADP, ATP carrier protein; ADP, ATP
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Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A; Title: Two distinct genes for ADP/ATP translocase
A; Reference number: A94197; MUID:88124845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987 A;Title: cDNA sequence of a human skeletal muscle ADP/ATP t. A;Reference number: A39891; MUID:88041149 A;Accession: A39891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: DNA sequences of two expressed nuclear genes A; Reference number: S03893; MUID:89236396 A; Accession: S03893
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A;Residues: 1-298 <LIA>
A;Cross-references: GB:J04982; NID:g178658; PIDN:AAA51736.1; PID:g178659
R;Cozens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
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A;Title: A human muscle adenine nucleotide
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A; Residues: 1-37 <HOU>
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A;Experimental source: clone pHMANT
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A;Residues: 1-298 <COZ>
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A; Residues: 1-15,'A',17-146,'RR',149,151-226,'L',228-298 <NEC>
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Best Local
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                                                                                                                                                                  Similarity
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A;Cross-references: EMBL:X70847
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: duplication; transmembrane protein
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP3>
submitted to the EMBL Data Library, February 1993 A;Description: A cDNA encoding an ADP/ATP carrier A;Reference number: S31935
                                                                                                        ADP,ATP carrier protein - African malaria mosquito
C;Species: Anopheles gambiae (African malaria mosquito)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #tex
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A;Molecule type: mRNA
A;Residues: 1-298 <COS>
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S31814
                                                               C; Accession: S31935; S31930
R; Beard, C.B.; Crews-Oyen,
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A; Accession: S31814
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hypothetical protein KO1H12.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_C;Caccession: T23207
R;McMurray, A.
submitted to the EMBL Data Library, December 1995
A;Reference number: 219707
A;Accession: T23207
A;Accession: T23207
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: EMBL:268218; PIDN:CAA92472.1; GSPDB:GN
A;Conetics:
A;Cenetics:
A;Genetics:
A;Genetics
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-301 <BEA>
A;Residues: 1-301 <BEA>
A;Cross-references: EMBL:Z21814; EMBL:Z21815
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: duplication; transmembrane protein
F;7-101/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;112-204/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;209-300/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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Best Local S
Matches 231
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Best Local
                                                                                                                                                                                                                                                                                                                                   Matches 207;
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                                                                                                                               LSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATS 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VRIPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLA 118
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                               LCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIY
                                                                                          AALWRGNLANVIRYFPTQALNFAFKDTYKNIFQKGLDKKKDFWKFFAGNLASGGAAGATS
                                                                                                                                                                                                          FLIDLASGGTAAAVSKTAVAPIERVKLLLQVQDASLTIAADKRYKGIVDVLVRVPKEQGY
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Similarity
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Score
Pred.
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Pred. No. 1.8e-84;
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No. 3
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.9e-97;
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submitted to the EMBL Data A; Reference number: Z20024 A; Accession: T25371
                                                                                                                                                    hypothetical protein T27E9.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Geisel, C.; Stellyes, L. submitted to the EMBL Data Library, December 1996 A;Description: The sequence of C. elegans cosmid
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A; Residues: 1-313 <GEI>
A; Cross-references: EMB
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A; Molecule type: DNA
A; Residues: 1-300 <WIL>
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A; Introns: 4/1; 191/2
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                                  A; Status: preliminary;
                                                                                                                 R; Lloyd, C
                                                                                                                                    C; Accession:
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70.9%;
                                                                                             Library,
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Pred. No. 2.7e-84;
                                      from GB/EMBL/DDBJ
                                                                                             November 1996
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A;Cross-references:

EMBL: 282059;

PIDN:CAB04874.1; GSPDB:GN00021;

CESP:T27E9.1

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A; Experimental source: C; Genetics:
A; Gene: CESP: T27E9.1
A; Map position: 3
A; Introns: 20/1; 41/3; 1
C; Superfamily: ADP, ATP o
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                                                                                                                                                           В
                                                                                                                                                                                    Q
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C;Superfamily: ADP,ATP carrier protein;
F;9-103/Domain: ADP,ATP carrier protein
                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-300 <LET>
A;Cross-references: EMBL:AF003141; NID:g2088732; PID:g2088738; PIDN:AAB54179.1; GSPDB:GN
A:Experimental source: strain Bristol N2; clone W02D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Le, T.; Weinstock, L.; Rifkin, L. submitted to the EMBL Data Library, May 1997 A;Description: The sequence of C. elegans co: A;Reference number: Z18308 A;Accession: T15206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein W02D3.6 - Caenorhabditis elegans C;Spectes: Caenorhabditis elegans C;Date: 20-Sep1999 #sequence_revision 20-Sep-1999 #tC;Accession: T15206
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                                                                                                                                                                                                                         Query Match
Best Local S
Matches 195
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Best Local
 179 VSVQGIIIYRAAYFGVYDTAKGML-PDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRR
                                 123
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                                                                                            ARVPKEQGYAAFWRGNLANVLRYFPTQALNFAFKDTYKKMFQEGIDKNKEFWKFFAGNLA 122
                                                                                                                                                                            TEQAISFAK---DFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCI 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPKEQGV 67
                                                                                                            VRIPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLA 118
                                                                                                                                                           TKEGFDYRKFLVDLASGGTAAAISKTAVAPIERVKLLLQVSDVSETVTADKKYKGIMDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIY 187
                                                             SGGAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAAYFGVYDTAKGML-PDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMQSGRKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSEWRGNLANVIRYEPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLIDLASGGTAAAVSKTAVAPIERVKLLLQVQDASKAIAVDKRYKGIMDVLIRVPKEQGV 71
                                 SGGAAGATSLCFVYPLDFVRTRLGADVGK-GVDREFQGLTDCFVKIVKSDGPIGLYRGFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -DILYKNTLDCAKKIIQNEGMSAMFKGALSNVFRGTGGALVLAIYDEIQKFL:
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69.2%;
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                                                                                                                                                                                                                         Score 993.5;
Pred. No. 2.7e
10; Mismatches
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Pred. No. 3 le-84;
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repeat homology <ACR>
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                                                                                                                                                                                                                                       2.7e-80;
                                                                                                                                                                                                                                                       DB 2;
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237
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A; Status: preliminary A; Molecule type: mRNA
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A; Molecule type: mRNA
A; Residues: 1-339 <HIL>
A; Residues: 1-339 <HIL>
A; Cross-references: GB:M76669; NID:g516596; PIDN:AAA33027.1; PID:g516597
C; Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat ho
C; Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F;38-134/Domain: ADP, ATP carrier protein repeat homology <ACP1>
F;144-235/Domain: ADP, ATP carrier protein repeat homology <ACP3>
F;241-329/Domain: ADP, ATP carrier protein repeat homology <ACP3>
                                                           N;Alternate names: ADP/ATP transporter C;Species: Plasmodium falciparum C;Date: 07-May-1995 #sequence_revision C;Accession: S68993; S51132 R;Hatin, I; Jaureguiberry, G, Eur. J. Biochem. 228, 86-91, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.Hilgarth, C.; Sauer, N.; Tanner, W. J. Biol. Chem. 266, 24044-24047, 1991 A;Title: Glucose increases the expression A;Reference number: A41677, MUID:92084708 A;Accession: A41677
A; Reference number: A; Accession: S68993
                   A; Title: Molecular characterisation of the ADP/ATP-transporter A; Reference number: S68993; MUID:95188918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADP, ATP carrier protein - Chlorella kessleri
C;Species: Chlorella kessleri
C;Date: 30-Jun-1992 #sequence_revision 30-Jun
C;Accession: A41677
                                                                                                                                                                                      ADP, ATP carrier protein - malaria parasite (Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
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Best Local Similarity 66.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAFVKDLLAGGTAGAISKTAVAPIERVKLLLQTQDSNPMIKSGQVPRYTGIVNCFVRVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADK--QYKGIVDCIVRIPK 63
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Pred. No. 7.3e-79;
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                                                                                                                          #text_change 09-Jun-2000
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A:Residues: 1-301 <HAT>
A:Residues: 1-301 <HAT>
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C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C:Keywords: duplication; transmembrane protein
F:6-102/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:112-203/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:209-301/Domain: ADP,ATP carrier protein repeat homology <ACP3>
Search completed: February 13, 2002, 09:32:09 Job time: 46 sec
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Best Local Similarity 61.8
Matches 183; Conservative
                                                                                              185 IIYRAAYEGYYDTAKGML-PDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMMQSG 243
                                                                                                                                                                                186 IVYRGSYFGLYDSAKALLFTNDKNTNIVLKWAVAQSVTILAGLISYPFDTVRRRMMMSG
                                                                                                                                                                                                                                                              127 AISLLIVYPLDFARTRLASDIGK-GKDRQFTGLFDCLAKIYKQTGLLSLYSGFGVSVTGI 185
                                                                                                                                                                                                                                                                                   125 ATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGI 184
                                                                                                                                                                                                                                                                                                                                         61.1%; Score 943; DB 2; Length 301; 61.8%; Pred. No. 7.8e-76; ative 45; Mismatches 62; Indels
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Result
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Maximum DB seq
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Perfect score:
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1454
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                                                                                                                                                                                      Score
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1543
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                                                                                                                                                                                                                                                                                                                                                                                          /SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1989.DAT:*
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385.502 Million cell updates/sec
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Human polypeptide
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Human polypeptide
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ADP/ATP carrier pr
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Antl protein. Mus
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| ţ                | 'n         | 44      | 43  | 42  | 41   | 40      | 39              | 38              | 37      | 36              | 35  | 34  | 33  | 32              | 31              | 30   | 29  | 28   | 27   | 26       | 25           | 24       | 23  | 22  | 21   | 20  | 19  | 18  | 17   | 16       | 15       | 14       | 13    | 12              |  |
|------------------|------------|---------|-----|-----|------|---------|-----------------|-----------------|---------|-----------------|-----|-----|-----|-----------------|-----------------|------|-----|------|------|----------|--------------|----------|-----|-----|------|-----|-----|-----|------|----------|----------|----------|-------|-----------------|--|
|                  | S          | 72.     | 84. | 85. |      | 88.     | បា              | S               | 58.     | •               | 67  | 67  | 79. | 79.             | 79.             | 88.  | 89. | 39.  | 39.  | 39.      | 42.          | 42.      | 42. | 42. | 42.  | 42. | 42. | 42. | 42.  | 42.      | 42.      | 42.      | 742.5 | 42.             |  |
|                  | 'n         | 7       | 7.  | 7.  | 8    | œ       |                 | .2              | 42.7    |                 | ω.  | ω.  |     | ٠               |                 |      | 4.  | 7.   | 7.   | 7.       | 8            | œ        | œ   | æ   | œ    | œ   | 8   | 8   | 8    | 8        | 8        | 8        | 48.1  | 8               |  |
| 077              | ٥          | 312     | 249 | 249 | 263  | 263     | 291             | 291             | 291     | 291             | 306 | 306 | 368 | 350             | 333             | 330  | 330 | 381  | 363  | 346      | 1027         | 1009     | 992 | 381 | 381  | 381 | 381 | 363 | 363  | 363      | 363      | 346      | 346   | 346             |  |
| 12               | 2          | 21      | 21  | 21  | 21   | 21      | 21              | 21              | 21      | 21              | 21  | 21  | 21  | 21              | 21              | 21   | 21  | 21   | 21   | 21       | 21           | 21       | 21  | 21  | 21   | 21  | 21  | 21  | 21   | 21.      | 21       | 21       | 21    | 21              |  |
| MUGZOTOS         | 0          | 281     | 394 | 206 | 9    | 129     | 169             | 129             | (4)     | 206             | 169 | 1O  | 390 | 390             | 390             | 393  | 2   | 177  | 177  | 177      | 386          | AAG38671 | 386 | 384 | 372  | 372 | 365 | 384 | 72   | 372      | AAG36576 | AAG38460 | 37    | 726             |  |
| viantoobata ciid | abidona in | idopsis | S   | S   | 8    | idopsis | Arabidopsis tha | Arabidopsis tha | idopsis | Arabidopsis tha | ເນ  | is  | ού  | Arabidopsis tha | Arabidopsis tha |      | is  |      | İS   |          | İS           |          |     | İS  | S    | Š   |     | İS  | S    | İS       | is       | İS       | S     | Arabidopsis tha |  |
| 0 ± ±0           | _          | 1       | 1   | _   | alia | alia    | alia            | alia            | alia    | alia            | 11  | 1   | 11  | alia            | alia            | alia | -   | alia | alia | $\vdash$ | $\mathbf{L}$ | -        | -   | _   | alia | _   | _   | _   | alia | $\vdash$ | alia     | alia     | alia  | alia            |  |

## ALIGNMENTS

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RESULT
AAY71033
diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder;
                                                                                                                                                                                                                                                                                  Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nootropic; antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
                                           03-NÓV-1998;
08-SEP-1999;
                                                                                                                                                                                                                       myoclonic
                                                                                                                                                                                                                                                                                                                                                                                                       Human adenine nucleotide translocator ANT3.
                                                                                          03-NOV-1999;
                                                                                                                          11-MAY-2000.
                                                                                                                                                          WO200026370-A2
                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                      29-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY71033 standard; Protein;
             (MITO-) MITOKOR
                                                                                                                                                                                                                       epilepsy red ragged fibre syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                           98US-0185904
99US-0393441
                                                                                            99WO-US25883
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                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC constructs. ANT is a nuclear encoded protein and a major component of conner mitochondrial membrane. It mediates transport of adenosine cdi/tri-phosphates across the mitochondrial inner membrane and also serves an important molecular component of the mitochondrial permeability can important molecular component of the mitochondrial permeability consists an important molecular component of the mitochondrial permeability or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for cregulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, parkinson's and untington's diseases, cancer, psoriasis, diabetes, dystonia, concer's hereditary optic neuropathy, schizophrenia, mitochondrial concephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative cdisorders, mitochondrial diabetes and deafness (MIDD), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is an adenine nucleotide translocator ANT3 from human brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anderson
Ghosh SS;
               Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
   caemokinetic;
                                                                                                Human polypeptide
                                                                                                                                    22-OCT-2001
                                                                                                                                                                                                 AAM39641 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant construct encoding adenine nucleotide polypeptide, useful e.g. in screening for potential against mitochondrial disease
                                                                                                                                                                                                                                                                                                                241
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                                                                                                                                                                                                                                                                              QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
                                                                                                                                                                                                                                                                                                                                                                             VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM 240
                                                                                                                                                                                                                                                                                                                                                                                                            gaagatslcfvypldfartrlaadvgksgterefrglgdclvkitksdgirglyqgfsvs 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 173-174; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                   (first entry)
   thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or ANT fusion
                                                                                                    SEQ
                                                                                                                                                                                                   Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  method to produce adenine nucleotide translocator fusion proteins using recombinant expression
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Pred. No. 2
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2.5e-157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     potential therapeutic agents
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                                                                                                                                                                                                                                                                                                           immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinyinhibin activity, chemotactic/chemokinetic activity, hemotactic/chemokinetic activity, hemotactic/chemokinetic activity, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang
Wang
Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUL-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                              specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; SEQ ID NO 2786; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JAN-2000;
25-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-)
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 181
                         181
                                                121
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                                                                                                61
                                                                                                                                                                                                        Local Similarity
                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to human nucleic acids (AAI57798-AAI61369) and encoded polypeptides (AAM38642-AAM42213) with nootropic.
GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
                                                                                                                                                          MTEQAISFAKDELAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-442253/47.
DB; AAI58797.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IJ,
QA,
                       VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM
                                                                                              IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120
                                                                                                                                             mtegaisfakdflaggiaaaisktavapiervklllqvqhaskqiaadkqykgivdcivr
                                                                                                                                                                                                                                                                                       disorders.
The sequence
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Wang :
Zhou
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2000US-0553317.

2000US-0598042.

2000US-0620312.

2000US-0653450.

2000US-0653450.

2000US-0653131.

2000US-0653131.
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u P,
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Wehrman T,
Goodrich
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Drmanac R
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Yang Y,
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                                                                                                                                                                                  The present sequence represents human adenine nucleotide translocator 3
(ANT-3) protein. ANT proteins are mitochondrial permeability
transition (MTP) pore components responsible for mediating transport
of ADP across the mitochondrial inner membrane. ANT proteins interact
with other mitochondrial core components e.g. cyclophilins to
regulate MPT. The present invention relates to a novel nucleic acid
expression construct comprising a promoter operably linked to a
cyclophyline encoding a mitochondrial pore component polypeptide
(e.g. ANT) fused to an energy transfer molecule (ETM) protein
(e.g. ANT) fused to an energy transfer molecule (ETM) protein
cyclopy area fluorescent protein (GFP) or a FLASH sequence). The novel
expression construct can alter mitochondrial membrane permeability
transition and/or alter the interaction between mitochondrial core
components. The methods are useful for screening for agents that alter
MFT and/or cell survival. These agents are useful for the prevention or
dysfunctional cell survival, such as Alzheimer's disease, diabetes
                              Query Match
Best Local S
Matches 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid expression constructs, useful for screening for an that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule.
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                                                                                                                                        mellitus, Parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke, hyperproliferative disorders e.g. cancer, and deafness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 2; 186pp; English
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                                                                                                              Sequence
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Velicelebi G,
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                                              Similarity
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                              0;
                              Score 1543;
Pred. No. 2.5
); Mismatches
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19-OCT-2000;
29-NOV-2000;
                 The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peripheral nervous system; neuropathy; central nervous system; Calzheimer's; Parkinson's disease; Huntington's disease; haemosta amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-JUL-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JAN-2000;
25-APR-2000;
                                                                                                                                                                 Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                                                                                                                                                           Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-AUG-2000;
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DB; AAI60583.
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Wang Z,
Zhou P,
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2000US-0662191.
2000US-0693036.
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Wehrman T,
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Yang Y,
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Zhang ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nootropic; antiParkinsonian; cytostatic; antiDabetic; antiConvulsant; neuroleptic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           system, such as peripheral nervous injuries, peripheral neuropathy localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as Immune system suppression, utilisation of the activities such as Immune system suppression,
  (MITO-) MITOKOR
                                                        03-NOV-1998;
08-SEP-1999;
                                                                                                                                     03-NOV-1999;
                                                                                                                                                                                                                                                   WO200026370-A2
                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                            myoclonic
                                                                                                                                                                                                                                                                                                                                                                                   diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;
Alzheimer's disease; Parkinson's disease; Huntington's disease; dyst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human adenine nucleotide translocator ANT2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY71032 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorders.
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99US-0393441
                                                                                                                                     99WO-US25883
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Pred. No. 2.8e-157;
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The patent discloses a method to produce adenine nucleotide translocator (ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine dlytri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, Leber's hereditary optic neuropathy, schizophrenia, mitochondrial conditions and stroke (MELAS), hyperproliferative diseases, mitochondrial function.
                                                                            disorders, mitochondrial diabetes and deafness (MIDD), and epilepsy red ragged fibre syndrome. The present sequence is adenine nucleotide translocator ANT2 from human brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant construct encoding adenine nucleotide translocator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-365619/31.
DB; AAD00520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45; Page 172-173; 175pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tide, useful e.g. in screening for potential therapeutic agents \min tochondrial disease .
298 AA;
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AAU01199
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Best Local S
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AAU01199
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                                                       VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM
                                                                                                                                                                   GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                                                 IPKEQGVLSFWRGNLANVIRYEPTQALNEAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                         vqgiiiyraayfgiydtakgmlpdpknthiviswmiaqtvtavagltsypfdtvrrrmmm
                                                                                                                                                         gaagatslcfvypldfartrlaadvgkagaerefrglgdclvkiyksdgikglyqgfnvs
                                                                                                                                                                                                      ipkeqevlsfwrgnlanviryfptqalnfafkdkykqiflggvdkrtqfwryfagnlasg
                                                                                                                                                                                                                                                                                                    Conservative
Protein;
                                                                                                                                                                                                                                                                                                             94.2%;
298
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Pred. No. 8.9e
13; Mismatches
                                                                                                                                                                                                                                                                                                              4; DB 21;
8.9e-148;
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Ωy Дb ρy

Вþ γ Вb

Human; adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin; mitochondrial permeability translition pore component; cell surviva mitochondrial core component; mitochondrial related disorder; cance Alzheimer's disease; diabetes mellitus; hyperproliferative disorde

survival;

adenine nucleotide translocator-2 (ANT-2) protein

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                   with other mitochondrial core components e.g. cyclophilins to
cregulate MPT. The present invention relates to a novel nucleic acid
expression construct comprising a promoter operably linked to a
component polypeptide
ce.g. any, fused to an energy transfer molecule (ETM) protein
ce.g. any, fused to an energy transfer molecule (ETM) protein
ce.g. any, fused to an energy transfer molecule (ETM) protein
ce.g. any, fused to an energy transfer molecule (ETM) protein
ce.g. any, fused to an energy transfer molecule (ETM) protein
cexpression construct can alter mitochondrial membrane permeability
transition and/or alter the interaction between mitochondrial core
components. The methods are useful for screening for agents that alter
treatment of diseases associated with altered mitochondrial function or
dysfunctional cell survival, such as Alzheimer's disease, diabetes
mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
cmitochondrial encephalopathy, lactic acidosis, stroke,
cmitochondrialerative disorders e.g. cancer, and deafness.
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                     Matches 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents human adenine nucleotide translocator-2 (ANT-2) protein. ANT proteins are mitochondrial permeability transport transition (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-NOV-1999;
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                                                                                                                   ipkeqevlsfwrgnlanviryfptqalnfafkdkykqiflggvdkrtqfwryfagnlasg
                                                                                                                                                                                                             IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
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                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                  94.2%;
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                                                                                                                                                                                                                                                                                                               Score 1454; DB 22;
Pred. No. 8.9e-148;
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                                                                                                                                                                                                                                                                                                                                 DB 22;
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                                                                                                                                                                Matches
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Best Local :
                                                                                                                                                                                                                                                                            The present sequence is the mouse Antl protein, the cDNA producing this polypeptide is cloned by screening a mouse heart cDNA library with the human Antl cDNA as a probe. The Antl cDNA sequence was determined by DNA Taq dideoxy terminator cycle sequencing. The Antl protein is encoded by the Antl locus, a nuclear gene on chromosome 8. This protein is required in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP which can then be converted into ATP. An Antl homozygous mutant would thus be defective in OXPHOS which results in disease in oxidative metabolism dependent tissues. This mouse Antl homozygous mutant can be used as a model system for fascioscapular humeral muscular dystrophy, hypertrophic cardiomyopathy, mopathy, lactic acidosis, etc. These model systems can be used to test possible therapeutic compounds which increase/mediate ATP and ADP exchange across the mitochondrial membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mice lacking heart-muscle adenine nucleotide translocator protein useful as model for mitochondrial myopathy and hypertrophic cardiomyopathy in animals and to test therapeutic compositions or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antl; Adenine nucleotide translocator; cloning; screening; DNA Taq dideoxy terminator cycle sequencing; oxidative phosphorylation; probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy; hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy; lactic acidosis; degenerative muscle disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW61169 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Graham BC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW61169;
                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYEM-) UNIV EMORY.
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GAAGATSLCEVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                   1998-286608/25
DB; AAV36479.
                                                                                                    mgdqalsflkdflaggiaaavsktavapiervklllqvqhaskqisaekqykgiidcvvr
                                           IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                         298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macgregor
                                                                                                                                                                                                                                                                   of ANT1.
                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0030017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39-40; 61pp; English
                                                                                                                                                                             91.5%;
                                                                                                                                                                19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 AA
                                                                                                                                                                             Score 1412;
Pred. No. 2
                                                                                                                                                                Mismatches
                                                                                                                                                               DB 19;
2.9e-143;
nes 15;
                                                                                                                                                                                          Length 298;
                                                                                                                                                                Indels
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RESULT
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              di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psociasis, diabetes, dystonia, Leber's hereditary optic neuropathy, schizophrenia, mitochondrial encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; adenine nucleotide translocator; ANT1; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; notropic; antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; antiParkinsonian; cytostatic; antidiabetic; screening; psoriasis; altielmer's disease; Parkinson's disease; Huntington's disease; dystonia, diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome.
                                                                                                                                                                                                          constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine
                                                                                                                                                                                                                                                           The patent discloses a method to produce adenine nucleotide translocator
                                                                                                                                                                                                                                                                                                Claim 44;
                                                                                                                                                                                                                                                                                                                             Recombinant construct encoding adenine polypeptide, useful e.g. in screening f against mitochondrial disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anderson CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-NOV-1998;
08-SEP-1999;
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     epilepsy
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DB; AAD00519.
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                                                                                                                                                                                                                                             proteins or ANT fusion proteins using recombinant expression
                                                                                                                                                                                                                                                                                               Page 172; 175pp; English.
       ragged fibre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleotide translocator
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99US-0393441.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wiley SE,
                                                                                                                                                                                                                                                                                                                                                                nucleotide translocator
                                                                                                                                                                                                                                                                                                                                              potential therapeutic agents
       sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miller SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Szabo
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RESULT
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Best Local
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The present sequence represents human adenine nucleotide translocator-1 (ANT-1) protein. ANT proteins are mitochondrial permeability transition (MTP) pore components responsible for mediating transport
                                                                                                                                                                                                                                                                                                                                      mitochondrial core co
Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                             mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                               Human adenine
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                                                                            New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
                                                                                                                            N-PSDB;
                                                                                                                                        WPI; 2001-291054/30.
                                                                                                                                                              Murphy AN, C
Velicelebi G,
                                                                                                                                                                                                                       03-NOV-1999;
                                                                                                                                                                                                                                              03-NOV-2000; 2000WO-US30535
                                                                                                                                                                                                                                                                                         WO200132876-A2
                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                        Human; adenine nucleotide translocator-1; ANT-1; MTP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU01198
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                                            Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60
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                                                                  energy transfer molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                           Fig
                                                                                                                                                              Clevenger W,
G, Davis RE;
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                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                     permeability transition pore component; cell su
core component; mitochondrial related disorder;
isease; diabetes mellitus; hyperproliferative di
                                                                                                                                                                                                                                                                                                                                                                                              nucleotide translocator-1 (ANT-1) protein
                                                                                                                                                                                                                       99US-0434354
                                            2;
                                           186pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translocator ANT1 from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89.8%;
87.2%;
                                            English.
                                                                                                                                                                          Wiley SE, Andreyev AY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1385.5; DE NO. 2e-140;
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                                                                                                                                                                                                                                                                                                                                                  cancer;
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RESULT 3
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Best Local Similarity 87.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynuclectide encoding a mitochondrial pore component polypeptide
                                                                                                                                                                                                               Moss; carbohydrate metabolism related protein; CMRP; sugar; cofactor; fine chemical production; carbohydrate; polysaccharide.
                                                                                                                                                                                                                                                        ADP/ATP carrier protein sequence #174.
                                                                                                                                                                                                                                                                                                                                      AAM00106 standard; Protein; 386 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mellitus, Parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke, hyperproliferative disorders e.g. cancer, and deafness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of ADP across the mitochondrial inner membrane.
              Frank M,
                        Lerchl J,
                                                    (BADI ) BASF PLANT SCI GMBH
                                                                                                        14-DEC-2000;
                                                                                                                                                                                       Physcomitrella
                                                                                                                                                                                                                                                                                   28-SEP-2001
                                                                               16-DEC-1999;
                                                                                                                                    21-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gaagatslcfvypldfartrlaadvgrr-agrefhglgdciikifksdglrglyggfnvs 179
            Freund A,
                          Renz A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297 AA;
                                                                                                        2000WO-EP12697
                                                                                                                                                                                                                                                                                 (first entry)
                                                                               99US-0171101
                                                                                                                                                                                       patens
           Ehrhardt T,
Duwenig E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.8%; Score 1385.5; DE 87.2%; Pred. No. 2e-140;
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            Reindl A,
Schmidt R,
           Cirpus P,
Reski R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22; Length
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                         Bischoff
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Sequence

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and/or enzymes. The nucleic acid molecules are suitable for modifying a carbohydrate production system in a host, e.g., microorganisms and plants. They are also useful to identify those DNA sequences and enzymes in other species which are useful to modify the biosynthesis of starch, cell wall polysaccharides and sugars. The nucleic acid molecules may be utilised in the genetic engineering of Corynebacterium glutamicum and the related Brevibactelum species and Acetobacter xylinum and Chlorella to make it a better or more efficient producer of one or more fine chemicals. Mutagenesis of one or more CMRPs may also result in CMRPs having altered activities which indirectly impact the production of one or more desired fine chemicals from plants. Primers AAH88707 - AAH80707
                                                                                                                                                                                                                                                                                                                                                                                         Included in the invention is a vector containing the CMRP cDNA, and a host cell transformed with the vector. The host cell (a microorganism, Corynebacterium or Brevibacterium, moss or algae or a plant cell) is useful for producing a fine chemical such as carbohydrates, cofactors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel moss nucleic acid molecules encoding a carbohydrate metabolism related protein useful for modulating production of fine chemicals such as carbohydrates, cofactors and enzymes from microorganisms and plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to nucleic acid molecules AAH88708 - AAH88796 isolated from Physcomitrella patens (a moss), which encode carbohydrate metabolism related proteins (CMRP) represented in AAM00022 - AAM00110.
                                                  are used in the sequencing of the CMRP cDNA sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 30; Page 131; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAH88792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-398155/42
386 AA;
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Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                Matches
 323
                                  242
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                                                                                                      183
                                                                                                                                      203
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                                                                                                                                                                                                                                                                           84
                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 157; Conserv
                                                                                             GIIIYRAAYFGVYDTAKG-MLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMQ
                                                                                                                                                                                                                         GVLSFWRGNLANVIRYEPTQALNEAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGA 125
                                                                                                                                                                                                                                                                           sgea···vkyngsmdafkqilakegakslfkgaganilravagagvlsgydqlq
                                                                giivyrglyfgiydslkpvvlvgnlegnflasfllgwgitigaglasypidtvrrrmmmt
                                                                                                                                   \verb|ssllfvysldyartrlandaksskkgggerqfnglvdvykktlatdgiaglyrgfaisca|\\
                                                                                                                                                     TSLCFVYPLDFARTRLAADV---GKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQ
                                                                                                                                                                                                       gmmslwrgntanviryfptgalnfafkdyfkslfgykkdk-dgywkwfagnlasggaaga
                                                                                                                                                                                                                                                                                                              SFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQ-HASKQIAADKQYKGIVDCIVRIPKEQ 65
                                SGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELK 295
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                48.6%;
                                                                                                                                                                                                                                                                                                                                              44; Mismatches
                                                                                                                                                                                                                                                                                                                                                              Score 749.5; DB 2
Pred. No. 5.5e-72;
                                                                                                                                                                                                                                                                                                                                                                                DB 22; Length 386;
                                                                                                                                                                                                                                                                                                                                                  84;
                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                     262
                                                                                                                                                                         182
                                                                                                                                                                                                           202
                                                                                                    241
                                                                      322
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Q

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RESULT 11
AAG36577
  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
Arabidopsis thaliana
                                                                   Arabidopsis thaliana protein fragment SEQ ID NO:
                                                                                                                                       AAG36577 standard;
                                                                                            18-OCT-2000
                                                                                                                  AAG36577;
                                                                                          (first entry)
                                                                                                                                       Protein;
                                                                                                                                        346
                                                                                                                                       B
                                                                     44845
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| •. | 29-JUN-1999;<br>30-JUN-1999;   | 9        | JUN-199       | JUN-199              | -199     | JUN-199  | JUN-199       | JUN-199  | JUN-199              | 70N-199     | JUN-199  | JUN-19      | JUN-199     | JUN-199          | -100        | -199        | 199         | -199           | 7 6 6       | -199        | JUN-199     | JUN-199     | ₊ ٺ         | MAY - 199   | MAY-199     | MAY-199     | MAY-199     | 9           | MAY-19        | MAY-199     | 199           | MAY - 199   | MAY-199     | MAY-199     | oΨ            | MAY-19      | -199        | APR-199     | APR-199     | 94     | APR-199     | APR-199 | 94                         | APR-199     | R-199       | oυ            | R-199       | -MAR-1         | -199<br>867-           | -FEB-199 | 25-FEB-2000;    | יי<br>די  |           | EP1033405-A2. |
|----|--------------------------------|----------|---------------|----------------------|----------|----------|---------------|----------|----------------------|-------------|----------|-------------|-------------|------------------|-------------|-------------|-------------|----------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|---------------|-------------|---------------|-------------|-------------|-------------|---------------|-------------|-------------|-------------|-------------|--------|-------------|---------|----------------------------|-------------|-------------|---------------|-------------|----------------|------------------------|----------|-----------------|-----------|-----------|---------------|
|    | 99US-0140991.<br>99US-0141287. | 014089   | 99US-0140354. | 014035               | 013981   | 013976   | 99US-0139463. | 013946   | 013946               | 013945      | 013945   | 013945      | 013945      | 013945           | 013949      | 013945      | 013945      | 013911         | 013854      | 013809      | 013772      | 013750      | 013752      | 013678      | 013639      | 013602      | 013562      | 013535      | 99US-0134941. | 013476      | 013437        | 013421      | 013421      | 013425      | 9905-0132487. | 013248      | 013248      | 013240      | 013204      | 013144 | 013051      | 013044  | 99US-0130077               | 012871      | 012823      | 99US-0126/85. | 012626      | 9905-0125788.  | 012318                 | 012182   | 2000EP-0301439. |           |           |               |
|    |                                |          |               |                      |          |          |               |          |                      |             |          |             |             |                  |             |             |             |                |             |             |             |             |             |             |             |             |             |             |               |             |               |             |             |             |               |             |             |             |             |        |             |         |                            |             |             |               |             |                |                        |          |                 |           |           |               |
|    |                                |          |               |                      |          |          |               |          |                      |             |          |             |             |                  |             |             |             |                |             |             |             |             |             |             |             |             |             | •           |               |             |               |             |             |             |               |             |             |             |             |        |             |         |                            |             |             |               |             |                |                        |          |                 |           |           |               |
|    |                                |          |               |                      |          |          |               |          |                      |             |          |             |             |                  |             |             |             |                |             |             |             |             |             |             |             |             |             |             |               |             |               |             |             |             |               |             |             |             |             |        |             |         |                            |             |             |               |             |                |                        |          |                 |           |           |               |
|    |                                |          |               |                      |          |          |               |          |                      |             |          |             |             |                  |             |             |             |                |             |             |             |             |             |             |             |             |             |             |               |             |               |             |             |             |               |             |             |             |             |        |             |         | -                          |             |             |               |             |                |                        |          |                 |           |           |               |
|    | סיטי                           | טי טי    | · O·          | ט יכ                 | סיו      | ייטי     | סינ           | ·O       | ייטי                 | ם כ         | ď        | ď,          | יי טי       | י ס              | סי כ        | P           | ~_ '        | יט             | סי כ        | יי          | י סי        | י סי        | ס יכ        | סי נ        | q           | · ط         | ייטי        | ם כ         | סי ו          | י פי        | יט            | סי כ        | קי          | ייטי        | סי ס          | ď           | יסי         | סינ         | P '         | יים    | g g         | ָּים.   | טי ט                       | סיי         | יי טיי      | ט יכ          | פינ         | יי טי          | טי כ                   | יפיו     | טי ט            | יי טי     | סיו       | סי סי         |
|    | بر بر                          | PR 07-   |               |                      | N        | N N      | ) N           | N        | N N                  | J K         | R 20     | N) I        | æ :<br>11:  | ָּבְּעָּ<br>בּיִ | מֹכּיל      | Ř 1.        | zi:         | <del>2</del> 2 | 10          | ж<br>0      | 0           | o (         | ٠ .         |             | 0           | ж :<br>О    | 0.0         | i xi        | 22            | χ :<br>2    | xi xi<br>N, N | 2 22        | R 2:        | χ̄ 2<br>2.1 | i zi          |             |             | 22          |             |        |             |         |                            |             | я ×         | ō R           | R           | <del>2</del> 2 | 7 R                    | × 1      |                 | 000       | R<br>O    | χ χ<br>0.0    |
|    | 3-SEP-1999;<br>5-SEP-1999;     | SEP-1999 | SEP-1999      | AUG-1999<br>AUG-1999 | AUG-1999 | AUG-1999 | AUG-1999      | AUG-1999 | AUG-1999<br>AUG-1999 | AUG-1999    | AUG-1999 | AUG-1999    | AUG-1999    | AUG-1999         | AUG-1999    | -1999       | AUG-1999    | AUG-1999       | AUG-1999    | AUG-1999    | AUG-1999    | -1999       | AUG-1999    | AUG-1999    | AUG-1999    | -1999       | AUG-1999    | AUG-1999    | JÜL-1999      | JUL-1999    | 666           | JUL-1999    | 1999        | 1999        | <br>  666<br> | 999         | 6667        | 6661        | 1999        | 666    | 1999        | 1999    | 999                        | 6661        | 6667        | 999<br>666    | 1999        | -JUL-1999      | -JUL-1999<br>-JUL-1999 | JUL-1999 | 1999<br>1999    | -JUL-1999 | -JUL-1999 | 999<br>966    |
|    | 99US-0153758.<br>99US-0154018. | -S06     | 9US-(         | -506                 | 9US-(    | -S06     | 9US-(         | 9US-(    | 9US-(                | 9US-0149929 | 9US-0    | 9US-0149722 | 9US-0149426 | 905-0149368      | 905-0148684 | 9US-0148565 | 9US-0148341 | 905-0148319    | 90S-0147935 | 9US-0147493 | 9US-0147416 | 9US-0147303 | 905-014/192 | 9US-0147302 | 908-0147204 | 9US-0147038 | 905-0146389 | 9US-0146386 | 9US-0145951   | 9US-0145919 | 905-0145918   | 9US-0145276 | 908-0145224 | 9US-0145218 | 908-          | 9US-0145089 | 9US-0145087 | 9US-0145088 | 9US-0145086 | -5116  | 9US-0144632 | 908-    | 90S-0144334<br>90S-0144335 | 9US-0144333 | 9US-0144332 | 90S-(         | 908-0144086 | 905-0          | 908-0                  | 908-0    | -Silb<br>-Silb  | 9US-0     | 905-      | 9US-(         |
|    |                                |          |               |                      |          |          |               |          |                      |             |          |             |             |                  |             |             |             |                |             |             |             |             |             |             |             |             |             |             |               |             |               |             |             |             |               |             |             |             |             |        |             |         |                            |             |             |               |             |                |                        |          |                 |           |           |               |

pathway;
promoter;

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RESULT 12
AAG37261
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                              VQGIIIYRAAYFGVYDTAK-----GMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVR
                                                                                                                                                                                                                                                                                      11v 336
                                                                                                                                                                                                                                               GATSLCFVYPLDFARTRLAAD----VGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                     KVI 298
                                                                                                                                                                                                                                {\tt gassllfvysldyartrlandakaakkggggrqfdglvdvyrktlktdgiaglyrgfnis}
                                                                                                                                                                                                                                                                                                                                                                                                         160;
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               990S-0154039
990S-0155139
990S-0155486
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52.8%;
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Pred. No. 2.7e-71;
5; Mismatches 77;
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                                                                                                                                               295
                                                                                                                                                                                                     235
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   25-FEB-1999;
05-MAR-1999;
23-MAR-1999;
23-MAR-1999;
25-MAR-1999;
06-APR-1999;
01-APR-1999;
01-MAY-1999;
01-JUN-1999;
01-JU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thaliana protein
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 9908-0125788.
9908-0126784.
9908-01287462.
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В δ В οy 밁 Ş Б Ş 밁 ą B ð.

S-0139461. S-0139462. S-0139463. S-0139750. S-0139763.

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Matches 160
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25-AUG-1999
26-AUG-1999
27-AUG-1999
28-SEP-1999
28-SEP-1999
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29-SEP-1999
21-OCT-1999
         181
                           161
                                           124
                                                           102
                                                                            64
                                                                                              44
                                                                                                              7
                                                                                           VQGIIIYRAAYFGVYDTAK-----
                       160;
                                                                                                                              h 48.1%;
Similarity 52.8%;
60; Conservative
                                                                                                                                                                990S-0149930.
990S-0150568.
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                                                                                                                               45;
                                                                                                                               Score 742.5;
Pred. No. 2.7e
15; Mismatches
-GMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVR
                                                                                                                                      .7e-71
                                                                                                                                                DB
                                                                                                                              77;
                                                                                                                                                21;
                                                                                                                               Indels
                                                                                                                                               Length
                                                                                                                                                346;
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                                                                                                                              Gaps
                           220
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         235
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C TISSUE-SKELETAL MUSCLE;

A Yamaguchi N., Kasai M.;

A Yamaguchi N., Kasai M.;

L Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.

C -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCH

C INNER MEMBRANE (BY SIMILARITY).

C -!- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.

R EMBL; AB009386; BAA23777.1; --

R InterPro; IPR001993; Mitoch_carrier.

R InterPro; IPR002067; Mit_carrier.

R InterPro; IPR002067; Mit_carrier.

R Pfam; PF00153; mito_carr; 3.

R PRINTS; PR00926; MITOCH_CARRIER; 3.

R PRINTS; PR00925; MITOCH_CARRIER; 3.

R PRINTS; PR00925; MITOCH_CARRIER; 3.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCH INNER MEMBRANE (BY SIMILARITY).

-!- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.

EMBL; X74510; CAA52616.1; --

EMBL; X74510; CAA52616.1; --

EMBL; R7240002; AAF64470.1; --

EMBL; RF2003791; AAF64470.1; --

REMBL; BC003791; AAF64470.1; --

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O62164;
O62164;
O1-NOV-1996 (TrEMBLrel. 01, Created)
O1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
O1-VOV-1996 (TrEMBLrel. 17, Last annotation update)
ADENINE NUCLEOTIDE CARRIER (ADENINE NUCLEOTIDE TRANSLOCASE 1) (SIMILAR TO SOLUTE CARRIER FAMILY 25 (MITOCHONDRIAL CARRIER, ADENINE NUCLEOTIDE TRANSLOCATOR), MEMBER 4).
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STRAIN=BALB/C; TISSUE=MUSCLE;
Laplace C., Costet P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inner membrane; Mitochondrion; SEQUENCE 298 AA; 32904 MW;
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             GAAGATSLCFVYPLDFARTRLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
                                                                                                                                                                                                                                             IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
                                                                                                                   IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASG
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etazoa; Chordata;
theria; Rodentia;
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Pred. No. 1.5e
10; Mismatches
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3A849FEAB0981462
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1.5e-126;
7;
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AB0981462 CRC64;
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; Murinae; Mus.
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RX MEDLINE-99083429; PubMed-9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT miura II., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT averigin and differentiation of the heteromorphic sex chromosomes
RT Z. W. X. and Yin the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase.";
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -:- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
CC INNER MEMBRANE (BY SIMILARITY).
CC EMBL. AB008457; BA35507.1; --
DR InterPro; IPR00193; Mitoch_carrier.
InterPro; IPR002007; Mit_carrier.
InterPro; IPR002007; Mit_carrier.
DR InterPro; IPR002007; Mit_carrier.
DR InterPro; IPR002007; Mit_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00784; MITOCARRIER,
DR PRINTS; PR00784; MITOCARRIER;
DR PRINTS; PR00784; MITOCHONDRIAL Transmembrane; Transport.
KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
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01-MAY-1999
01-MAY-1999
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QSGRKGAEIMYSGTIDCWKKIARDEGSRAFFKGAWSNVLRGMGGAFVLVLYDELKKYI
                             QSGRKGAD IMYTGTVDCWRK IAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV
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Neobatrachia;
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Pred. No. 1.2e
23; Mismatches
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a; Ranoidea;
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les 16;
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REDLINE=99083429; pubMed=9866197;

RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

RT asex linked gene, App/ATP translocase.";

RI M. X., and Y in the frog Rana rugosa, inferred from the sequences of RT a sex linked gene, App/ATP translocase.";

RI Mol. Biol. Evol. 15:1612-1619(1998).

C-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL CINCHONDRIAL CI
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01-MAY-2000
01-MAY-2000
01-JUN-2001
                                                                                  Q9PRH2;
01-MAY-2000
01-MAY-2000
01-JUN-2001
                   Rana rugosa (Frog).
Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; N
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Eukaryota; Metazoa; Chordata;
                                                                     ADP/ATP TRANSLOCASE.
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                      Neobatrachia;
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Pred. No. 1.2e-118;
                                    Craniata; Vertebrata;
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annotation update)
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Ranidae; Rana
                    Eutelecstomi;
Ranidae; Rana
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A mira I. Ohtani H. Nakamura M., Ichikawa Y., Saitoh K.;
T. Whe origin and differentiation of the heteromorphic sex
T. W. X. and Y in the frog Rana rugosa, inferred from the
T a sex-linked gene, ADP/ATP translocase.";

Mol. Biol. Evol. 15:1612-1619(1998).

- I. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITO
C INMER MEMBRANE (BY SIMILARITY).

C INGER MEMBRANE (BY SIMILARITY).

C - SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.

EMBL; AB008460; BAA36510.1; -.

R EMBL; AB008459; BAA36508.1; -.

R EMBL; AB008459; BAA36509.1; -.

R INterPro; IPR002067; Mit_Carrier.

R InterPro; IPR002067; Mit_Carrier.

R InterPro; IPR002067; Mit_Carrier.

R InterPro; IPR002030; Mit_Carrier.

R Pfam; PF00153; mito_carr; 3.

R Pfam; PR00784; MTUNCOUPLING.

R PROSITE; PS00715; MITOCARRIER; 3.

PROSITE; PS00715; MITOCARRIER; 3.

PROSITE; PS00715; MITOCARRIER; 3.
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Best Local
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01-OCT-2000
01-JUN-2001
Crawford M.J., Khosrowshahian F., Varmuza S.L., Liversage "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Spec Dynamic Patterns of Expression During Development."; Submitted (FEB-2000) to the EMBLYGENBAMK/DDBJ databases.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOC INNER MEMBRANE (BY SIMILARITY).
                                                                                                                                 Xenopus laevis (Airican craweu rroy),
Eukaryota; Metazoa; Chordata; Craniata; Ver
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                   ANT1.
                                                                                                                 Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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                                                                                            SEQUENCE
                                                                                                                                                                                               ADENINE
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2001 (TrEMBLrel. 17, Las
NUCLEOTIDE TRANSLOCASE.
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Pred. No. 2.3e
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B0E225E867599A06 CRC64;
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ia; Pipoidea; Pipidae;
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RA Chen 2., Fair J.A., Batterham P.;

RA Chen 2., Fair J.A., Batterham P.;

RT "A cDNA clone encoding the ADP/ATP translocase of Lucilia cuprina.";

RT "A CDNA clone encoding the EMBL/GenBank/DDBJ databases.

CC :INTER MEMBRANE (DEC-1999) to the EMBL/GenBank/DDBJ databases.

CC :INTER MEMBRANE (BY SIMILARITY).

CC :INTER MEMBRANE (BY SIMILARITY).

CC :INTER MEMBRANE (BY SIMILARITY).

CC :INTER MEMBRANE (BY SIMILARITY).

CR INTERPOOLOGY; AAF32322.1; -.

DR InterPro; IPR001993; Mitoch_Carrier.

DR InterPro; IPR002097; Mit_Carrier.

DR Pfam; PF00153; mito_carri.

DR Pfam; PF00153; mito_carri.

DR PRINTS; PR00215; MITOCH_CARRIER; 3.

DR PRINTS; PR00215; MITOCH_CARRIER; 3.

Inner membrane; Mitochondrion; Transmembrane; Transport.

KW Inner membrane; Mitochondrion; Transmembrane; Transport.

SEQUENCE 300 AA; 33036 MW; 5459DF0BA0E2E742 CRC64;
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Lucilla cuprina (Greenbottle fly) (Australian sheep blowfly).

Lucilla cuprina (Greenbottle fly) (Australian sheep blowfly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musco
Oestroidea; Calliphoridae; Lucilia.
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2001 (TrEMBLrel. 17,
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PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MITOCALLING.
PROSITE; PS00215; MITOCH_CARRIER; 3.
Inner membrane; Mitochondrion; Transmembrane; Transport.
SEQUENCE 298 AA; 32940 MW; 91B740133751877F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPKEQGELSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MTDAAISFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKHYKGIMDCVVR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPKEQGFVSFWRGNLANVIRYFPTQALNFAFKDKYKKIFLDNVDKKTQFWRYFAGNLASG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257;
                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
79.9%; Score 1241.5; 78.7%; Pred. No. 3.94; ive 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.0%;
86.2%;
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Last annotation update)
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3; Mismatches
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                               9e-106;
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                                                      DB 5;
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Gaps
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Q91336;
01-NOV-1996 (TrEMBLrel. 0
01-MAY-1999 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
ADP/ATP TRANSLOCASE.
                                                                                                                                                                                                                                  PROSITE;
Inner meml
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97398141; PubMed-9256066; Cai Q., Greenway S.C., Storey K.B.; Cai Q., Greenway S.C., Storey K.B.; Pifferential regulation of the mitochondrial ADP/ATP translocase gene in wood frogs under freezing stress."; Biochim. Biophys. Acta 1353:69-78(1997).
                                                                                                                                                                                                                                                                      EMBL; U44832; AAA97882, 2; -
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; Mito_carr; 3.
                                                                                                                                                                                                                                                                                                                                                   Cai Q., Storey K.B.; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases -i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rana sylvatica (wood frog).
Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; Ne
                                                                                                                                                                                                                                             PRINTS; PR00926; MITOCARRIER. PROSITE; PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                          Local Similarity nes 233; Conser
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                                                                                                                                                                                                                                                                                                                         INNER MEMBRANE (BY SIMILARITY)
SIMILARITY: TO THE MITOCHONDRI
MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                                                IPKEQGELSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
                                                                                                       MTDAANSFAKDFLAGGVAAAISKTAVAPIERVKLLVQVQHASKQITADKQYKGIMDCVVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MMQSGRKATEIIYKNTLHCWATIAKQEGTGAFFKGAFSNVLRGTGGAFVLVLYDEIKKFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MMQSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSVQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASGGAAGATSLCFVYPLDFARTRLAADTGKGGQREFTGLGNCLAKIFKSDGLVGLYRGFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVRIPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPKEQGFISFWRGNLANVIRYFPTQALNFGFKDKYKKIFLDNVDKRTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSVQGIIIYRAAYFGFYDTARGMLPDPKNTPIYISWAIAQVVTTVAGIVSYPFDTVRRRM
                                                                                                                                                                                                                         membrane; Mitochondrion; NCE 317 AA; 35005 MW;
                                                                                                                                                        Conservative
                                                                                                                                                                      79.5%;
85.7%;
                                                                                                                                                                                                                                                                                                                            MITOCHONDRIAL
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10,
17,
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Last
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                                                                                                                                                       Score 1234.5; DB 13
Pred. No. 1.9e-105;
Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata;
eobatrachia; Ranoidea;
                                                                                                                                                                                                                        Repeat; Transmembrane; 5F66B7ED8D5CEB72 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence update) annotation updat
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                                                                                                                                                                                  DB 13;
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Ranidae; Rana
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                                                                                                                                                                                   317;
                                                                                                                                                        1.
                                                                                                                                                        Gaps
                          179
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RESULT
044094
ID 04
AC 04
DT 01
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Best Local S
Matches 226
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EMBL; AF025798; AAB8783.1; -.

F1yBase; FBgn0023292; Dpse\sesB.

InterPro; IPR001993; Mitoch_carrier.

InterPro; IPR002067; Mit_carrier.

Pfam; PF00153; mito_carr; 3.
044094
044094;
01-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       044093;
01-JUN-1998
01-JUN-1998
01-JUN-2001
                                                                                                                                                                                                                                                                                               PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
Inner membrane; Mitochondrion; Repeat; Transmembrane;
NON_TER 288 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila pseudoobscura (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          044093
                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7237;
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                                                           ATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGII 184
                                                                                                                                  ATSLCFVYPLDFARTRLAADTGKGGQREFTGLGNCLTKIFKSDGLVGLYRGFGVSVQGII
                                                                                                                                                                                                                                                                                      288 AA;
(TrEMBLrel.
                                                                                                                                                                                                                                          Conservative
                 PRELIMINARY;
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79.6%; Pre
ative 25;
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06, Last sequence up
17, Last annotation
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Created)
                                                                                                                                                                                                                                                   Score 1183; DB 5; Pred. No. 8.9e-101;
                 PRT;
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Best Local S
Matches 226
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-: SUBCELLULAR LOCATION: INTEGRAL MEMB INNER MEMBRANE (BY SIMILARITY).

-: SIMILARITY: TO THE MITOCHONDRIAL CA EMBL; AF025799; AAB87884.1; -.

FlyBase; FB9n0023237; DSub\sesB.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PR00153; Mitoch_CARRIER.
PROSTTE; PR00926; MITOCARRIER.
3.
PRINTS; PR00926; MITOCARRIER.
                                                                                                                                                                    062526 PRELIMINARY; PRT; 307 AA.
062526; 01-AUG-1998 (TrEMBLrel. 07, Created) .
01-AUG-1998 (TrEMBLrel. 07, Last sequence update) .
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.
Amanatides P.G., Scherer S.E., Li
                                        SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                              ANT2 PROTEIN.
ANT2 OR CG1683.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation updat ADP/ATP TRANSLOCASE (FRAGMENT).
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                                                                              NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inner membrane; Mitochondrion; NON_TER 288 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              QGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAG
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79.6%;
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Galle
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Best Local :
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InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; Mito_carrier.
PRINTS; PR00153; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_2.
SEQUENCE 307 AA; 33744 MW; 3D6B3DFD82061COC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhang Y.Q., Davis A.W., Roote J., Ashburner M.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003484; AAF47956.1; -.
EMBL; Y10618; CAA71629.1; -.
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                                      DIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
                                                                                                                             RAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMQSGRKGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIPKEQG 66
                                                                                                                                                                                                                       SLCFVYPLDFARTRLAADVGKGGNREFNGLIDCLMKVIKSDGPIGLYRGFIVSVQGIVIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFLMDFMMGGVSAAIAKTAVAPIERVKLILQVQEVSKQIAADQRYKGIVDCFIRIPKEQG 76
                                                                                                   RAAYFGFYDTCRDFLPNPKSTPFYVSWAIAQVVTTVAGIASYPFDTVRRRMMMQSGLKKS
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73.8%;
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Pred. No. 2e-97;
3; Mismatches 43
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Q9H0C2;
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InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCARRIER; 3.
Inner membrane; Mitochodation; Repeat; Transmembrane; Transport.
SEQUENCE 304 AA; 33306 MW; 51FD0D7D6B654880 CRC64;
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-!- SIMILARITY: TO THE MITOCHONDRIAL
EMBL; D83069; BAA11765.1; -.
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Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
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"Expression of a gene for major mitochondrial protein, ADP/ATP
translocase, during embryogenesis in the ascidian Halocynthia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGA 122
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(TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 17,
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Pred. No. 9.6e-97;
8; Mismatches 54;
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P91410; 01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO ADP/ATP TRANSLOCASE.
T01B11.4
Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton I., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
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                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans
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                                                                                                                                  STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
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Pred. No. 3.2
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                                                                                                                                                               Eukaryota; Metazoa; Nemata Rhabditidae; Peloderinae; NCBI_TaxID=6239;
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PROSITE; PS00215; MITOCARRIER; 3.
Inner membrane: Micochondrion; Repeat; Transmembrane; '
SEQUENCE 313 AA; 34356 MW; CF07C473A719CCB6 CRC64;
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-i- SIMILARITY: TO THE MITOCHONDRIAL CARRIER EMBL; U80931; AAB38001.1;
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                                                                   SEQUENCE FROM N.A. Mcmurray A.;
                                                                                                                                                                                                                                                                          Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAYFGVYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQSGRKGA
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1 (JAN-1997) to
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IPR002067; Mit_carrier.
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No. 4.4e-88;
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortinore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaudjan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PF00153; mito_carrier.
PRINTS; PF0025; MITOCARRIER:
PROSITE; PF00215; MITOCH_CARRIER; 3.
Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
SEQUENCE 313 AA; 34384 MW; D1E455DDB463C984 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 368:32-38(1994).

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).

-!- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=94150718; PubMed=7906398;
Wilson R., Ainscough R., Anderson
263 DVLYKNTLDCAVKIIKNEGMSAMFKGALSNVFRGTGGALVLAIYDEIQKFI 313
                                                                                    205
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                                                                                                                                                                                           128 LCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYR 187
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                                                                                                                                                                                                                                                                                                                                                                       8 FLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIPKEQGF 67
                                                                                AAYFGVYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQSGRKGA 246
                                                                                                                                                                                                                                                                                     LSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGATS 127
                    DIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
                                                                                                                                                                                                                                                            AALWRGNLANVIRYFPTQALNFAFKDTYKNIFQKGLDKKKDFWKFFAGNLASGGAAGATS 144
                                                                                                                                                                                                                                                                                                                                                FLIDLASGGTAAAVSKTAVAPIERVKLLLQVQDASLTIAADKRYKGIVDVLVRVPKEQGY 84
                                                                                                                                                                       LCFVYPLDFARTRLAADVGKANEREFKGLADCLVKIAKSDGPIGLYRGFFVSVQGIIIYR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   67.2%; Score 1043.5; DB 5; Length 313; 69.4%; Pred. No. 6.8e-88; 1tive 37; Mismatches 49; Indels 3;
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Search completed: February 13, 2002, 09:34:14 Job time: 171 sec

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| 246          | 248.5        | 258.5        | 263.5        | 265.5       | 267.5        | 279.5        | 286          | 291         | 292         | 292.5        | 295          |
| 15.8         | 16.0         | 16.6         | 17.0         | 17.1        | 17.2         | 18.0         | 18.4         | 18.7        | 18.8        | 18.8         | 19.0         |
| 436          | 324          | 326          | 695          | 325         | 322          | 676          | 587          | 675         | 332         | 307          | 322          |
| 1            | -            | 1            | <u> </u>     | 1           | <u> </u>     | _            | _            | H           | Н           | _            | Ľ            |
| BT1_MAIZE    | PMT_YEAST    | YEO8_SCHPO   | CMC1_DROME   | BMCP_HUMAN  | BMCP_MOUSE   | CMC2_MOUSE   | CMC3_CAEEL   | CMC2_HUMAN  | GDC_HUMAN   | YO7L_YEAST   | GDC_RAT      |
| P29518 zea m | P32332 sacch | 013805 schiz | Q9va73 droso | 095258 homo | Q9z2b2 mus m | Q9qxx4 mus m | Q19529 caeno | Q9ujs0 homo | P16260 homo | Q99297 sacch | P16261 rattu |
| zea mays (m  | saccharomyc  | schizosacch  | phila        | homo sapien | nusculu      | nusculu      | rhabdi       | sapien      | homo sapien | naromyc      | s norv       |

## ALIGNMENTS

|  | R R R R R R R R R R R R R R R R R R R | RNL TARKSTLT   |
|--|---------------------------------------|--|
| SEQUENCE OF 1-37 FROM N.A.  TISSUE-Liver; MEDLINE-B8124845; Pubmed-2829183; Houldsworth J., Attardi G.; "Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in adult human liver."; Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988) |                                       | LT 1 ADT1_HUMAN STANDARD; PRT; 298 AA. ADT1_HUMAN STANDARD; PRT; 298 AA. ADT1_HUMAN STANDARD; PRT; 298 AA. P1235; 01-OCT-1989 (Rel. 12, Created) 01-NOV-1990 (Rel. 16, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) ADP,ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1). SLC25A4 OR ANT1. HOMO SEPIENS (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE-89236396; Pubmed=2541251; COZENS A.L., Runswick M.J., Walker J.E.; "DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP translocase."; J. Mol. Biol. 206:261-280(1989). |

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EMBL; J03593; AAA36751.1; -.
EMBL; J04982; AAA51736.1; -.
PIR; A28116; A28116.
PIR; A39891; A39891.
PIR; S03893; S03893.
                                                        Q05952;
Q1-FEB-1994 (Rel. 28, Created)
Q1-FEB-1994 (Rel. 28, Last sequence update)
Q1-AUG-2001 (Rel. 40, Last annotation update)
ADP, ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP) ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP) (ADP) (ANT 1)
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Eukaryota;
            Rattus norvegicus (Rat)
Eukaryota; Metazoa; Cho
                                                      SLC25A4 OR ANT1.
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PRINTS; PR00927; ADPTRNSLCASE.
PROSITE; PS00215; MITOCH_CARRIER;
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InterPro; IPR001993; Mitoch_carrier.
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Pred. No. 1.8e-131;
2; Mismatches 2;
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"Isolation and characterization of cDNA clones and a genomic encoding rat mitochondrial adenine nucleotide translocator.";
Biochim. Biophys. Acta 1152:192-196(1993).
-!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS TH
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Interpro; IPR002067; Mit_carrier.
Interpro; IPR001993; Mitoch_carrier.
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DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS
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QSGRKGADIMYTGTVDCWRKIAKDEG
                        QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV
                                                             VQGIIIYRAAYEGVYDTAKGMLPDPKNVHIFVSMMIAQSVTAVAGLLSYPFDTVRRRMM
                                                                                                      GAAGATSLCFVYPLDFARTRLAADVGKGSSQREFNGLGDCLTKIFKSDGLKGLYQGFSVS
                                                  VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQSVTAVAGLVSYPFDTVRRRMM
                                                                                                                                                        IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASG
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PR00927; ADPTRNSLCASE.
;; PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                           Similarity
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Pred. No. 5.1e-126;
9; Mismatches 7;
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01-FEB-1996 (Rel. 33, Last sequence update)
10-FEB-1996 (Rel. 33, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ADP,ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)
                                                                                                                                                                                                                                                                                                                                                    EMBL; U27315; AAC52837.1; -. MGD; MGI:1353495; S1c25a4. InterPro; IPR002067; Mit_carrier. InterPro; IPR001993; Mitoch_carrier. Pfam; PF00153; mito_carr; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97059403; PubMed=8903724; Ellison J.W., Li X., Francke U., "Rapid evolution of human pseudoa
                                                                                                                                                              REPEAT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                          Multigene
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                                                m. Genome 7:25-30(1996).
FUNCTION: CATALYZES THE EXCHANGE MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
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             IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
                                                            MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASG
                                                MGDQALSFLKDFLAGGTAAAVSKTAVAPTERVKLLLQVQHASKQTSAEKQYKGTIDCVVR
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'57BL/6; TISSUE=Brain;
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Rodentia;
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                                                                                                Score 1457.5; DB 1
Pred. No. 3.4e-125;
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Sciurognathi;
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                     EMBL; M13783; AAA30363.1
EMBL; M24102; AAA30768.1
PIR; A03181; XMBO.
PIR; A24822; A24822.
PIR; A43646; A43646.
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ADT1_BOVIN
P02722;
21-JUL-1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=89229093; PubMed=2540808; Powell S.J., Medd S.M., Runswick M.J. Powell S.J., Medd S.M., Runswick M.J. Powell S.J., Medd S.M., Runswick M.J. Town Louis for mitochondrial differences in various tissues."; Biochemistry 28:866-873(1989).
                                                                                                                                                  between
the Euro
                                                                                                                                                                                                                                                               MEDLINE=89229093;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pec
Bovidae; Bovinae; Bos.
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20-AUG-2001 (Rel. 40, Last annotation update)
ADP_ATP CARRIER PROTEIN, HEART ISOFORM T1 (ADP/ATP TRANSLOCASE
(ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).
                                                                                                             use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
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                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 207-297 FROM N.A. MEDLINE-86295775; PubMed-3017341; Rasmussen U.B., Wohlrab H.;
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European Bioinformatics Institute
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SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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D., Eulitz M., Klingenberg M
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l ADP/ATP translocase expressed
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Matches 280
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE-Brain;
STRAIN=97059403; PubMed-8903724;
MEDLINE-97059403, Li X., Francke U., Sh
A Ellison J.W., Li X., Francke U., Sh
                                                                                                                                                                                                                                                                                                      ADT2_MOUSE STANDARD,

ADT2_MOUSE STANDARD,

P51881; Q61311;

01-OCT-1996 (Rel. 34, Created)

01-OCT-1996 (Rel. 34, Last sequence update)

20-AUG-2001 (Rel. 40, Last annotation update)

ADP,ATP CARRIER PROTEIN, FIBROBLAST ISOFORM (
...PMINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2).
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SEQUENCE FROM N.A. TISSUE=Skeletal muscle; Sheldon J.G.; Thesis (1995), Universi
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PRINTS; PR00926; MITOCARRIER;
PRINTS; PR00927; ADPTRNSLCASE.
PROSITE; PS00215; MITOCH_CARRIER;
                                                                                          Mamm.
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Mammalia; Eutheria;
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COSEAS OR ANIA.
AS musculus (Mouse).
Arvota; Metazoa; Chordata; Comercia; Rodentia; S
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REPEAT
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SEQUENCE
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PRINTS; PR00927; ADPTRNSLCASE.
PROSITE; PS00215; MITOCH_CARRIER;
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EMBL; U10404; AAA19009.1;
EMBL; X70847; CAA50196.1;
MGD; MGI:1353496; Slc25a5
                                                                                                                                                                                                                                                                                                                                                                                                                               or send an
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                                                                                GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
                                                                                                         SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EW
        QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
                                            VQGIIIYRAAYEGVYDTAKGMLPDPKNVHIEVSWMIAQSVTAVAGLLSYPEDTVRRRMM
                                                                       GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFKGLGDCLVKIYKSDGIKGLYQGFNVS
QSGRKGTDIMYTGTLDCWRKIARDEGSKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
                                   VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIFISWMIAQSVTAVAGLTSYPFDTVRRRMMM
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IPR001993; Mitoch_carrier.
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O1-FEB-1995 (Rel. 31, Created)
O1-FEB-1995 (Rel. 31, Last sequence update)
O1-FEB-1995 (Rel. 31, Last sequence update)
O1-FEB-1995 (Rel. 40, Last annotation update)
ADP,ATP CARRIER PROTEIN, FIBROBLAST ISOFORM (ADP/ATP TRANSLOCASE (ADENINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. Then the by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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-I- FUNCTION: CATALXZES THE EXCHANGE OF ADP AND ATP ACROSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00927; ADPTRNSLCASE.
PROSITE; PS00215; MITOCH_CARRIER;
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                                                                                                                                                                                                                                                                                                     SEQUENCE
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Mammalia; Eutheria; Rodentia;
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                       IPKEQGELSFWRGNLANVIRYEPTQALNEAFKDKYKQLELGGVDRHKQFWRYFAGNLASG 120
                                                                                                           MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
                                                                                        {\tt MTDAAVSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR}
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IPR001993; Mitoch_carrier.
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Sciurognathi; Muridae;
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ADT2.HUMAN STANDAKD;
P05141; 043350;
13-AUG-1987 (Rel. 05, Created)
13-AUG-1994 (Rel. 30, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
ADP,ATP CARRIER PROTEIN, FIBROBLAST ISOFORM (ADP/ATP TRANSLOCASE)
ADP,ATP CARRIER PROTEIN, FIBROBLAST ISOFORM (ADP/ATP TRANSLOCASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cloning a J. Biol. [2]
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no wav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Nag: Chen C.N., Su Y., Baybayan P., Siruno A., Nag: Mazzarella R.A., Schlessinger D., Chen E.Y.; Submitted (JUN-1996) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 growth-regulated J. Biol. Chem. 20
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MEDLINE=90375457; PubMed=2168878;
MEDLINE=90375457; PubMed=2168878;
MEDLINE=90375457; PubMed=2168878;
MEDLINE=Placenta;
The human fibroblast adenine nucleotide transcription and sequence.";
                                                                                                                                                                                                                                                             "Two distinct genes for ADP/ATP translocase are level in adult human liver."; Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988)...- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND MITOCHONDRIAL INNER MEMBRANE.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular cloning of a cDNA for a human growth-regulated.":
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                                                                                                                                  DOMAIN: COMPOSED SIMILARITY: BELON
                                                                                                                                                                                          INNER MEMBRANE
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BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY
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Primates;
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to the EM
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Best Local Similarity
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P12236;
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                     P12230;
01-OCT-1989 (Rel. 12, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP
         Homo
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                  SLC25A6 OR ANT3.
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InterPro; IPR001993; Mitoch_carrier.
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EMBL; J02683; AAA35579.1; --
EMBL; L78810; AAB39266.1; --
EMBL; AC004000; AAB96347.1; --
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         sapiens (Human)
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                                                                                                                                                                                                                 MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQVKGIIDCVVR 60
                                                                                                                                       QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
                                                                                                                                                                           GAAGATSLCEVYPLDEARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
                                                                                                                                                                                                                                                                   IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKOLFLGGVDRHKQFWRYFAGNLASG 120
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Craniata; Vertebrata;
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G -> E (IN REF. 2).
R -> L (IN REF. 4 AN
V -> G (IN REF. 5).
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(See http://www.isb-sib.ch/announce/
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N REF. 4 AND 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 level in adult human liver.";
Proc. Natl. Acad. Sci. U.S.A: 85:377-381(1988)
-!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AN
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InterPro; IPR001993; Mitoch_carrier.
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NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Two distinct genes for ADP/ATP translocase are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
            121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: HOMODIMER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN: COMPOSED OF
                                                                                                                                                                                                                                                                                                                                                                                             S03894;
B28116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INNER MEMBRANE
GAAGATSLCEVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
                                                                                                                                                                                                                                                                                                                                                                          403000;
                                                                      IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                         IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                          PR00927; ADPTRNSLCASE.; PS00215; MITOCH_CARRIER;
                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol.
                                                                                                                                                                                                                                                                                                                                PR00926; MITOCARRIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translocase
                                                                                                                                                                                                             family.
12
73
117
117
176
214
273
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298
                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             в28116
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                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                 Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=2829183;
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87.2%;
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Pred. No. 1.2e-1
1; Mismatches
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(POTENTIAL)
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RESULT ADT3\_BO

\_BOVIN

P32007; ADT3

\_BOVIN

SLC25A6 OR ANT3

NCBI\_TaxID=9913; Bovidae; Ş В õ Вþ

GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS

180

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241 240 181 180 121

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Query Match
Best Local
              Multigene family.
TRANSMEM 12
TRANSMEM 73
TRANSMEM 117
TRANSMEM 176
TRANSMEM 214
TRANSMEM 273
REPEAT 112
REPEAT 120
SEQUENCE 298 AA;
                                                          Mitochondrion;
Local Similarity
               Ą,
                                                         Inner membrane;
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134
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               1C34E7DF6EDE4061 CRC64
                              (POTENTIAL)
                                                         Repeat;
1380.5; DB 1
No. 3.3e-118;
                                                         Transmembrane;
   μ,
   Length
                                                         Transport;
    298
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the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by are entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
"Two bovine genes for mitochondrial ADP/ATP translocase differences in various tissues.";
Biochemistry 28:866-873(1989).
-I- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ADP,ATP CARRIER PROTEIN, ISOFORM T2 (ADP/ATP
NUCLECTIDE TRANSLOCATOR 3) (ANT 3).
                                                                                                                                                                                                     PFAMM, PF00153; mito_carr; 3.
PRINTS; PR00925; MITOCARRIER;
PROSITE; PS00215; MITOCH_CARRIER;
PROSITE; PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                   PIR; B43646; B43646.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=89229093; PubMed=2540808;
                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN: COMPOSED SIMILARITY: BELON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: INTEGRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MITOCHONDRIAL INNER MEMBRANE. SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria;
                                                                                                                                                                                                                                                                                               AAA30769.1;
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BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY
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actyla; Ruminantia; Pecora;
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                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                         Zhang Y.Q., Davis A.W., Submitted (JAN-1997) to
                                                                                                                                                                                                                                                                                                                                                           melanogaster shows a ADP/ATP translocases.
                                                                                                                                                                                                                 STRAIN=OREGON-R;
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=94350065;
                                                                                                                                                                                                                                                                                                                                                J. Mol. Evol.
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This SWI

EMBL; M24103;

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Matches
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brrandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-ffannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Bouck D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;

Pterygota; Neoptera; Endopterygota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADT_DROME STANDARD: PRT; 297 AA. 026365; 026254; P91614; 09VZ70; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) ADP,ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hutter P., Karch F.; "Molecular analysis of a candidate gene for the isolation between sibling species of Drosophila. Experientia 50:749-762(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSLOCATOR) (ANT) (STRESS SESB OR A/A-T OR CG16944.
                                                                                                                                                                                                                                                                                 MEDLINE=20196006; PubMed=10731132;
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Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guann P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McHillow G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Syler E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Wanng Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worlev K.C. Wn D Vanc Scheenbach J.,
Matches
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"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
-i- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).
                                                                                                                                                           CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00927; ADPTRNSLCASE.
PROSITE; PS00215; MITOCH_CARRIER; 3.
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InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; S43651; AAB23114.1; -. EMBL; S71762; AAB31734.3; -. EMBL; Y10618; CAA71628.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents
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                        78.0%;
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                        8.3e-103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSLOCATOR) (ANT).

Anopheles gambiae (African malaria mosquito).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
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01-NOV-1997 (Rel: 35, Last annotation update)
ADP,ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE)
                                                                 PRINTS; PR00927; ADPTRNSLCASE.
PROSITE; PS00215; MITOCH_CARRIER;
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SUBUNIT: HÖMODIMER (BY SIMILARITY)
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"Glucose increases the expression of the glyceraldehyde-1-phosphate dehydrogenase of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the c
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Chlorella kessleri.
Eukaryota: Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ADP,ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE)
Pfam; PF00153; mito_carr; 3. PRINTS; PR00926; MITOCARRIER. PRINTS; PR00927; ADPTARSICASE PROSITE; PS00215; MITOCH_CARR:
                                                                                     PIR; A41677; A41677.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                             EMBL; M76669; AAA33027.1; -.
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01-AUG-1992 (Rel. 23, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation updat
ADP, ATP CARRIER PROTEIN (ADP/ATP TRANSLOCAS
TRANSLOCATOR) (ANT).
                                                            between
the Euro
                                                                                                                                                                                                     Sharpe J.A., Day A.; "Structure, evolution and expression of the mitochondrial ADP/ATP translocator gene from Chlamydomonas reinhardtil.";
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Eukaryota; Viridiplantae; Chlorophyta;
Chlamydomonadaceae; Chlamydomonas.
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01-AUG-1992 (Rel.
                                use by non-profit institutions as long modified and this statement is not removed.
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                                              s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                               . Gen. Genet. 237:134-144(1993)
FUNCTION: CAMALYZES THE EXCHEN
MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: INTEGRA
                                                                                                           DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                         INNER MEMBRANE.
DOMAIN: COMPOSED
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          requires a license agreement (See an email to license@isb-sib.ch).
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                                                                                      SEQUENCE FROM N.A.
STRAIN-MUTIND-FR7205034;
STRAIN-91322533; PubMed-1863785;
MEDLING-91322533; PubMed-1863785;
Winning B.M., Day C.D., Sarah C.J., L.
"Nucleotide sequence of two cDNAs encurrent control of two control of two control of two control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control
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ADT1_MAIZE
      STRAIN-CV.
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Panicoideae; Andropogoneae; 20
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

College: Donocae: PACC Cl
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01-AUG-1992 (Rel. 23, La
20-AUG-2001 (Rel. 40, La
ADP, ATP CARRIER PROTEIN
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InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                SEQUENCE OF 59-387 FROM N.A.
                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4577;
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Nucleic Acids Res. 13:5857-5867(1985).
-!- FUNCTION: CATALYZES THE EXCHANGE OF
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"Two genes encode the adenine nucleotide translocator of mitochondria. Isolation, characterisation and expression
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InterPro; IPR001993; Mitoch_carrier.
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PIR; S05199; S05199.
PIR; S14876; S14876.
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Baker A., Leaver C.J.;
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Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
MITOCHONDRIAL INNER MEMBRANE.
-I- SUBUNIT: HOMODIMER (BY SIMILARITY).
-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Couzin N., Trezeguet V., Saux A.L., Lauquin G.J.M.;

"Cloning of the gene encoding the mitochondrial adenine nucleotide carrier of Schizosaccharomyces pombe by functional complementation Saccharomyces cerevisiae.";

Gene 171:113-117(1996).
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01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ADP,ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE)
TRANSLOCATOR) (ANT).
ANC1 OR SPBC530.10C.
                                                                                       Interpro; IPR002067; Mit_carrier.
Interpro; IPR001993; Mitoch_carrier.
Pfam; PF00153; Mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00927; ADPTRNSLCASE.
PROSITE; PS00215; MITOCH_CARRIER; 2.
                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                               EMBL; AL023634; CAA19176.1; -. HSSP; P04002; IATF.
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## ALIGNMENTS

ADP,ATP carrier protein T1 - human

ADP,ATP carrier protein T1 - human

N,Alternate names: mitochondrial ADP,ATP translocase 1

C;Species: Homo sapiens (man)

C;Date: 17-Mar-2000 #sequence\_revision 17-Mar-2000 #text\_change 17-Mar-2000

C;Accession: A44778; S03893; A39891; A28116

R;Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, J. Biol. Chem. 264, 13998-14004, 1989

A;Title: A human muscle adenine nucleotide translocator gene has four exons, is locat A;Reference number: A44778; MUID:89340499

A;Reference number: A44778; MUID:89340499

A;Rolecule type: DNA

A;Residues: 1-298 <LIA>

A;Residues: 1-298 <LIA>

A;Residues: CB-104082; NID:6178658; DIDN:AAA51736 1: DID:6178659

| F;110-202/Domain: ADP,ATP carrier protein repeat homology <acp2></acp2>                | crier pr |
|--|----------|
| F;5-99/Domain: ADP,ATP carrier protein repeat homology <acp1></acp1>                   | crier pr |
| F;2-298/Product: ADP,ATP carrier protein #status predicted <mat></mat>                 | rrier pr |
| C; Keywords: duplication; homodimer; mitochondrion; transmembrane protein              | rrier pr |
| C; Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology     | rrier pr |
| A; Map position: 4935-4935   | al prote |
| A;Cross-references: GDB:119680; OMIM:103220  | rrier pr |
| A;Gene: GDB:ANT1; T1   | rrier pr |
| C; Genetics:   | rrier pr |
| A; Experimental source: liver  | rrier pr |
| A;Cross-references: GB:J03593; NID:g339724; PIDN:AAA36751.1; PID:g339725               | anslocas |
| A; Residues: 1-37 <hou></hou>  | crier pr |
| A; Molecule type: mRNA   | rrier pr |
| A; Accession: A28116   | al prote |
| A;Reference number: A94197; MUID:88124845  | rrier pr |
| A;Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level i  | rrier pr |
| Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988  | al prote |
| R;Houldsworth, J.; Attardi, G.   | al prote |
| A; Experimental source: clone pHMANT   | al prote |
| A;Cross-references: GB:J02966; NID:g339919; PIDN:AAA61223.1; PID:g339920               | al prote |
| A; Residues: 1-15, 'A', 17-146, 'RR', 149, 151-226, 'L', 228-298 < NEC>                | rrier pr |
| A; Molecule type: mRNA   | rrier pr |
| A;Status: preliminary  | rrier pr |
| A;Accession: A39891  | rrier pr |
| A;Reference number: A39891; MUID:88041149  | rrier pr |
| A; Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a lea | rrier pr |
| Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987                                      | rrier pr |
| R; Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.                      | cleotide |
| A; Residues: 1-298 <coz></coz>   | rrier pr |
| A; Molecule type: DNA  | 1 4      |
| A; Status: not compared with conceptual translation                                    | _        |
| A;Accession: S03893  |          |
| A;Reference number: S03893; MUID:89236396  |          |
| A; Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP |          |
| J. Mol. Biol. 206, 261-280, 1989   |          |
| R;Cozens, A.L.; Runswick, M.J.; Walker, J.E.   |          |
| A;Cross-references: GB:J04982; NID:g178658; PIDN:AAA51736.1; PID:g178659               | inted,   |
| A; Restones: 1-290 Stray   |          |

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C;Accession: 160173
R;Shinohara, Y:; Kamida, M.; Yamazaki, N.; Terada, H.
Biochim. Biophys. Acta 1152, 192-195, 1993
A;Title: Isolation and characterization of cDNA clones
A;Reference number: 160173; MUID:94002161
A;Accession: 160173
A;Stetero.
                                                                                                                                                                                                                                                                                                                                                                                       A;Introns: 37/3; 200/1; 247/1
A;Introns: 37/3; 200/1; 247/1
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein rC;Keywords: duplication; transmembrane protein
E;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
E;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
E;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
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                  VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQSVTAVAGLVSYPFDTVRRRMM
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                                                    VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMM 239
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                                                                                                                                                                                                                                                                                                      Score 1466.5; DB 2;
pred. No. 2.7e-125;
pred. No. 7;
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Pred. No. 9.8
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                                                                                                                 C:Species: Bos primigenius taurus (cattle)
C;Date: 14-Nov-1983 #sequence_revision 22-Uul-1994 #text_change
C;Accession: A43646; A2482; A03181; A61343; S69369
R;Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
Blochemistry 28, 866-873, 1989
B;Title: Two bowine genes for mitochondrial ADP/ATP translocase
A;Reference number: A43646; MUID:89229093
A;Accession: A43646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein; (Keywords: duplication; transmembrane protein F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision
C;Accession: S37210
           R;Rasmussen, U.B.; Wohlrab, H.
Biochem. Biophys. Res. Commun. 138, 850-857,
A;Title: Bovine cardiac mitochondrial ADP/AT
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                                                                     A; Cross-references: GB: M24102; NID: g529414;
                                                                                     A; Molecule type: mRNA
A; Residues: 1-298 < POW>
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A; Residues: 1-298 <LAP>
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mitochondrial ADP/ATP-carrier:
822; MUID:86295775
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Pred. No. 5e-
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                                                                      PIDN: AAA30768.1;
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R.Obstudes. W.; Masson, K.; Kalinna, S.

Bur. J. Blochem. 227, 730-733, 1995

A:Title: [(3)H]7-azido-4-isopropylacridone labels Cys159 of the bovine mitochondrial in the control of the control of the control of the control of the control of the mitochondrial in the cytosol of the control of the mitochondrial in the cytosol of the cytosol of the bovine mitochondrial in the cytosol of the cytosol of the cytosol of the mitochondrial in the cytosol of the cytosol of the mitochondrial cytosol of the cytosol of the mitochondrial in the cytosol of the cytosol of the mitochondrial of the cytosol of the cytosol of the mitochondrial membrane

G:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the mitochondrial membrane

G:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytosol of the cytoso
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N;Alternate names: mitochondrial ADP,ATP translocase 2 (;Speciles: Homo sapiens (man) C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change C;Accession: A29132; C28116 R;Battini, R.; Ferrari, S.; Kaczmarek, L.; Calabretta, B.; Chen,
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A; Molecule type: mR
A; Residues: 208-298
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A; Residues: 2-51,'x',53-70,'x',72-109,'x',111-298
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                                                                                                                                                                                                                                                                                                                                                                                       QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMM 239
                                                                                                                                                                                                                                                                                                                                                   QSGRKGADIMYTGTVDCWRKIAKDEGPKAFFKGAWSNVLRGMGGAFVLVLYDEIKKFV
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Pred. No. 1.4e
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nes 9;
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ADP, ATP carrier protein T3 - human
N; Alternate names: ADP, ATP carrier protein T2 (misider
C; Species: Homo sapiens (man)
C; Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #t.
C; Accession: S03894; B28116
R; Cozens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A; Title: DNA sequences of two expressed nuclear genes
A; Reference number: S03893; MUID:89236396
A; Accession: S03894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GDB:125190; OMIM:300150
A;Map position: Xq13-Xq26
A;Nap position: Xq13-Xq26
A;Note: there may be some confusion in the assignment of sequences for GDB:ANT2
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F;510-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Houldsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A; Title: Two distinct genes for ADP/ATP translocase are expre
A; Reference number: A94197; MUID:88124845
A; Accession: C28116
A; Accession: C28116
A; Accession: G28116
A; Residues: 47-65, 'G', 67-110, 'L', 112-161, 'G', 163-298 <HOU>
A; Residues: 47-65, 'G', 67-110, 'L', 112-161, 'G', 163-298 <HOU>
A; Cross-references: GB:J03591; NID:g339720; PIDN:AAA36749.1;
A; Experimental source: clone pHAT3
C; Genetics:
R:Houldsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A;Title: Two distinct genes for ADP/ATP translocase
A;Reference number: A94197; MUID:88124845
A;Accession: B28116
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A;Title: Molecular cloning of a cDNA for a h
A;Reference number: A29132; MUID:87166056
A;Accession: A29132
A;Accession: A29132
A;Recule type: mRNA
A;Residues: 1-298 <BATY
A;Cross-references: GB.J02683; NID:g179246;
A;Cross-references: GB.J02683; NID:g179246;
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A; Residues: 1-298 <COZ>
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                                                                                                                                                              conceptual translation
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                                               expressed at the
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A:Cross-references: GDB:125184; OMIM:300151; OMIM:403000
A:Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
A;Mote: there may be some confusion in the assignment of sequences for GDB:ANT2.C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein F;2-298/Product: ADP,ATP carrier protein #status predicted <MATP F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                  A;Cross references: GB:M24103; NID:g529416; PIDN:AAA30769.1; PID:g529417 C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat ho C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1> F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP3> F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADP.ATP carrier protein T2 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
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                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-298 < POW>
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R;Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
Biochemistry 28, 866-873, 1989
A;Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently A;Reference number: A43646; MUID:89229093
A;Accession: B43646
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A; Residues: 36-104, 'R',106, 'A',109-298 <HOU>
A; Cross-references: GB:J03592; NID:g339722; A; Experimental source: liver
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
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IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR 60
                                         MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60
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                                                                                                                                        88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.2%;
                                                                                                                   21;
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Pred. No. 5.8e
21; Mismatches
                                                                                                                                        Score 1380.5; DB 2; Pred. No. 1.6e-117;
                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIDN:AAA36750.1;
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N;Alternate names: adenine nucleotide C;Species: Mus musculus (house mouse) C;Date: 06-Tan-1995 #sequence_revision C;Accession: S31814 R;Costet, P.; Laplace C
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A;Residues: 1-298 <COS>
A;Cross-reférences: EMBL:X70847
A;Cross-reférences: EMBL:X70847
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier proțein repeat homology
C;Keywords: duplication; transmembrane protein
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP3>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
submitted to the EMBL Data Library, February 1993 A;Description: A cDNA encoding an ADP/ATP carrier A;Reference number: S31935
                                                               ADP,ATP carrier protein - African malaria mosquito C;Species: Anopheles gambiae (African malaria mosquito) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #tex C;Accession: S31935; S31936 R;Beard, C.B.; Crews-Oyen, A.E.; Collins, F.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNP
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A; Accession: S31814
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR 60
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                                                                                                                                                                                                                                                                                                                                                                                    VQGIIIYRAAYFGYYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMM
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Pred. No. 2e-116;
B; Mismatches 1
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                     mosquito
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                       Anopheles
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                  gambiae
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A;Accession: S31935
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-301 <BEA>
A;Cross-references: EMBL:Z21814; EMBL:Z21815
A;Cross-references: EMBL:Z21814; EMBL:Z21815
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein
C;Keywords: duplication; transmembrane protein
F;7-101/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;112-204/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;209-300/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                              A:Molecule type: DNA
A:Residues: 1-313 <GEI>
A:Residues: 1-313 <GEI>
A:Cross-references: EMBL:U80931; PIDN:AAB38001.1; GSPDB:GN00022;
A:Experimental source: strain Bristol N2; clone T01B11
C:Genetics:
A:Gene: CESP:T01B11.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein T01811.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C;Accession: T25850
R;Geisel, C.; Stellyes, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, December 1996 A;Description: The sequence of C. elegans cosmid T01B11. A;Reference number: Z20099 A;Accession: T25850
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T25850
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A; Introns: 4/1; 191/2
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                                                                                                        KSEVMYKNTLDCWVKIGKQEGSGAFFKGAFSNVLRGTGGALVLVFYDEVK 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IYRAAYFGYYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQSGRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSLCFVYPLDFARTRLAADVGRRA-QREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGII 184
LCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYR 187
                                    AALWRGNLANVIRYFPTQALNFAFKDTYKNIFQKGLDKKKDFWKFFAGNLASGGAAGATS
                                                       LSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGATS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IYRAAYFGCFDTAKGMLPDPKNTSIFVSWAIAQVVTTASGIISYPFDTVRRRMMQSWPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIGAFCGGNLANVIRYFPTQALNFAFKDVYKQVFLGGVDKNTQFWRYFLGNLGSGGAAGA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGA 125
                                                                                                                                                                                                                                                                              ADP, ATP
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                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                          carrier protein; ADP, ATP carrier
                                                                                                                                                                                                  67.3%;
69.8%;
                                                                                                                                                                                 36;
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Pred. No. 6e-96;
26; Mismatches 4
                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                    Score 1045.5; DB 2; Pred. No. 3.8e-87;
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                                                                                                                                                                                 Mismatches
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C; Accession: Tz
C; Accession: Tz
                                                                   A;Reference number: Z20024
A;Accession: T25371
A;Status
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
A;Molecule type: DNA
A;Residues: 1-300 <WIL>
A;Cross-references: EMBL:Z82059; PIDN:CAB04874.1; GSPDB:GN00021; CESP:T27E9.1
                                                                                                                                                           hypothetical protein T27E9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C;Accession: T25371
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A; Introns: 4/1; 191/2
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A; Residues: 1-313 <WIL>
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                                                           A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                             R; Lloyd, C
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Best Local Similarity
Matches 202; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLIDLASGGTAAAVSKTAVAPIERVKLLLQVQDASLTIAADKRYKGIVDVLVRVPKEQGY 84
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69.48;
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Pred. No. 5.8e-87;
7; Mismatches 49;
                                                                                                                        November 1996
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A; Introns: 20/1; 41/3;
C; Superfamily: ADP, ATP
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A;Description: The sequence of C. elegans cosmid W02D3
A;Reference number: Z18308
A;Accession: T15206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change
C;Accession: TJ15206
R;Le, T.; Weinstock, L.; Rifkin, L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-300 <LET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein W02D3.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
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Best Local S
Matches 192
                                                                                                                                                                                                                                                                                                                                    Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology; 9-103/Domain: ADP,ATP carrier protein repeat homology <ACR>
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Best Local
188 AAYFGVYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQSGRKGA 246
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                                                                  LCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYR 187
                                                                                                     AAFWRGNLANVLRYFPTQALNFAFKDTYKKMFQEGIDKNKEFWKFFAGNLASGGAAGATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAYFGMFDTAKMVFASDGQKLNFFAAWGIAQVVTVGSGILSYPWDTVRRRMMMQSGRK--
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                                   LCFVYPLDFVRTRLGADVGKGVDREFQGLTDCFVKIVKSDGPIGLYRGFFVSVQGIIIYR
                                                                                                                                         LSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGATS 127
                                                                                                                                                                              FLVDLASGGTAAAISKTAVAPIERVKLLLQVSDVSETVTADKKYKGIMDVLARVPKEQGY 71
                                                                                                                                                                                                                                                      192;
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                                                                                                                                                                                                                                                                   Score 1005.5; DB Pred. No. 1.5e-83;
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                                                                                                                                                                                             C;Date: 07-May-1995 #sequence_revision
C;Accession: S68993; S51132
                                                                                                                                                                                                                                C; Species: Plasmodium falciparum
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                                                                                                                                                                                                                                                N; Alternate names: ADP/ATP transporter
                                                                                                                                                                                                                                                                 ADP, ATP carrier protein - malaria parasite
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R;Hilgarth, C.; Sauer, N.; Tanner, W.
J. Biol. Chem. 266, 24044-24047, 1991
A;Title: Glucose increases the expression
A;Reference number: A41677; MUID:92084708
A;Accession: A41677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: GB:M76669; NID:g516596; PIDN:AAA33027.1; PID:g516597 C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat hc;Keywords: duplication; homodimer; mitochondrion; transmembrane protein F;38-134/Domain: ADP,ATP carrier protein repeat homology <ACP1> F;144-235/Domain: ADP,ATP carrier protein repeat homology <ACP2> F;241-329/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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C;Species: Chlorella Kessleri
C;Date: 30-Jun-1992 #sequence_revision 30-Ju
C;Accession: A41677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-339 <HIL>
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                    KGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
                                                                                  IYRAAYFGYYDTAKGML-PDPKNVHIFYSWMIAQSYTAVAGLLSYPFDTVRRRMMMQSGR
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Pred. No. 1.4e-80;
0; Mismatches 65
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A;Cross-references: EMBL:X83551; NID:g623334; PIDN:CAA58541.1; PID:g623335 C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homo C;Keywords: duplication; transmembrane protein A; Molecule type: mRNA A; Residues: 1-301 <HAT> A; Reference number: A; Accession: S68993 R;Hatin, I.; Jaureguiberry, G. Eur. J. Biochem. 228, 86-91, 1995 Eur. Whlecular characterisation of the A:Reference number: S68993; MUID:95188918 A; Status: preliminary ADP/ATP-transporter CDNA repeat homology from the

01-Sep-1995

#text\_change 09-Jun-2000

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                                                   244 KG-ADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
247 KGKEEIQYKNTIDCWIKILRNEGFKGFFKGAWANVIRGAGGALVLVFYDELQKLI 301
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AAG39398 AAG12916 AAG16974 AAG20659 AAG39399

AAG39400 AAG12918 AAG16976 AAG28188 AAG28189

ALIGNMENTS

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| (MITO-) MITOKOR. |    | 03-NOV-1998: 98US-0185904. | 03-NOV-1999; 99WO-US25883. | 11-MAY-2000. |   | WO200026370-A2. | ношо вартеня. |     | myoclonic epilepsy red ragged fibre syndrome. | mitochondrial diabetes and deafness; hyperproliferative disorder; | mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; | diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; | Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia; | antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; | antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; | mitochondrial permeability transition; neuroprotective; nootropic; | adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; | Human; adenine nucleotide translocator; ANT1; mitochondria; ADP; ATP; |   | Human adenine nucleotide translocator ANT1. |   | 29-AUG-2000 (first entry) |   | AAY71031; | notited acamaata, frocern, 401 mm. | TD ANYTIO21 standard Drotoin 207 AA | 1001 L |

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SUMMARIES

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CC constructs. ANT is a nuclear encoded protein and a major component of
CC cinner mitochondrial membrane. It mediates transport of adenosine
CC di/rti-phosphates across the mitochondrial inner membrane and also serves
CC as an important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial pore activity, for treating diseases associated
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
CC epilepsy red ragged fibre syndrome. The present sequence is an
CC adenine nucleotide translocator ANTI from human brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                             Human; adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin; mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer
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                Alzheimer's disease; diabetes
                                                                                             Human adenine
                                                                                                                                                                                         AAU01198 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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Ghosh SS;
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DB; AAD00519.
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Pred. No. 1.3e-173;
                mellitus;
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                hyperproliferative disorder
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polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MPT and/or cell survival. These agents are useful for the prevention or treatment of diseases associated with altered mitochondrial function or
                                                                                                                                                                                                                                                                                                               (ANT-1) protein. ANT proteins are mitochondrial permeability transition (MTP) pore components responsible for mediating trof ADP across the mitochondrial inner membrane. ANT proteins with other mitochondrial core components e.g. cyclophilins to
                                                   dysfunctional cell survival, such as Alzheimer's disease, diabetes mellitus, Parkinson's disease, Huntington's disease, schizophrenia mitochondrial encephalopathy, lactic acidosis, stroke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule
                                                                                                                                                                                                                                                                          regulate MPT. The present invention relates to a novel nucleic expression construct comprising a promoter operably linked to
                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents human adenine nucleotide translocator-l (ANT-1) protein. ANT proteins are mitochondrial permeability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murphy AN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-NOV-1999;
                                     hyperproliferative disorders e.g. cancer, and deafness.
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297 AA;
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G, Davis RE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
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Sequence

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                         SGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV
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Matches 279
                                                                                                                                                                                                                                                                                                                               the Antl locus, a nuclear gene on chromosome 8. This protein is require in mitochondrial oxidative phosphorylation (DXPHOS), as it imports ADP which can then be converted into ATP. An Antl homozygous mutant would thus be defective in OXPHOS which results in disease in oxidative metabolism dependent tissues. This mouse Antl homozygous mutant can be used as a model system for fascioscapular humeral muscular dystrophy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mice lacking heart-muscle adenine nucleotide translocator protein useful as model for mitochondrial myopathy and hypertrophic cardiomyopathy in animals and to test therapeutic compositions or
                                                                                                                                                                                                                                                                                      hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These mod systems can be used to test possible therapeutic compounds which increase/mediate ATP and ADP exchange across the mitochondrial membrane
                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide is cloned by screening a mouse heart cDNA library with the human Antl cDNA as a probe. The Antl cDNA sequence was determined by DN Taq dideoxy terminator cycle sequencing. The Antl protein is encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antl; Adenine nucleotide translocator; cloning; screening; DNA Taq dideoxy terminator cycle sequencing; oxidative phosphorylation; probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy; hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy; lactic acidosis; degenerative muscle disease.
                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAV36479
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                                                                                                              GAAGATSLCFVYPLDFARTRLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
                                                                     IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
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                                                                                                                                                                                     93.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   is the mouse Antl protein, the cDNA producing d by screening a mouse heart cDNA library with probe. The Antl cDNA sequence was determined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GR,
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                                                                                                                                                                        Score 1457.5; DB 19
Pred. No. 2.2e-162;
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          The patent discloses a method to produce adenine nucleotide translocator CC (ANT) proteins or ANT fusion proteins using recombinant expression CC constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine CC di/tri-phosphates across the mitochondrial inner membrane and also serves CC as an important molecular component of the mitochondrial permeability CC transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is an order of the nucleotide translocator ANT? from human brain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nootropic; antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia
                                                                                                                                                                                                                                                                                                                                                             Claim 45;
                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide, useful e.g. in screening
against mitochondrial disease -
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                                                                                                                                                                                                                                                                                                                                                           Page 172-173; 175pp; English.
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99US-0393441.
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The present sequence 2 from human brain.
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The present sequence represents human adenine nucleotide translocator-2 (ANT-2) protein. ANT proteins are mitochondrial permeability transition (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact
                                                                                                                                Disclosure;
                                                                                                                                                                                                   New nucleic acid expression constructs, useful for screening for a that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-NOV-1999;
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Best Local
                                                                                                                                                            mitochondrial permeability transition; neuroprotective; nootropic; antiparkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzhelmer's disease; Parkinson's disease; Huntington's disease; dystonia; diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic peniloge; and deafness; hyperproliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MPT and/or cell survival. These agents are useful for the prevention on treatment of diseases associated with altered mitochondrial function or dysfunctional cell survival, such with altered mitochondrial survival, such with altered mitochondrial survival, such with altered mitochondrial survival, such with altered mitochondrial survival, such with altered mitochondrial survival, such with altered mitochondrial encephalopathy, lactic acidosis, stroke, hyperproliferative disorders e.g. cancer, and deafness.
                                                                                                                                                                                                                                                                        Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nootropic;
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                                                                                                                                                                                                                                                                                                                                             Human adenine nucleotide translocator ANT3.
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                                                                                                                     Homo sapiens
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N-PSDB; AAD00521.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clevenger W, Wiley SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1385.5; DB 21
Pred. No. 6.1e-154;
P1; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Miller SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                          The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as Alzheimer's, parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, hamostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                     Wang
                                                                                                                                                                                                                                                                                                                                                                                                  Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                        C.N.S disorders.
Note: The sequence specification.
                                                                                                                                                                                                                                                              Example 4;
                                                                                                                                                                                                                                                                                         such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-DEC-2000;
Sequence
                                                                                                                                                                                                                                                                                                      Novel nucleic acids and
                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; nootropic; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                       , r
TY
                                                                                                                                                                                                                                                                                                                                 2001-442253/47.
DB; AAI58797.
                                                                                                                                                                                                                                                                                        ucleic acids and polypeptides, useful for treating central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                       Liu C,
Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                             HYSEQ INC
                                                                                                                                                                                                                                                              SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0662191.
2000US-0662191.
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                                                                                                                                                                                                                                                                                                                                                                       Asundi V, Ch
Wehrman T, X
Goodrich R,
                                                                                                                                                                                                                                                            NO 2786; 10078pp; English
                                      data
                                      for
                                      this
                                                                                                                                                                                                                                                                                                                                                                                   Chen R,
                                                                                                                                                                                                                                                                                                                                                                         Drmanac
                                      patent did not
                                                                                                                                                                                                                                                                                                                                                                                   Xue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic;
                                                                                                                                                                                                                                                                                                                                                                         RT;
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Yang
                                      form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                     g Υ,
                                      part
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Zhang
                                      of the printed
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Qy
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                                                                                                                      Query Match
Best Local S
Matches 260
                    121
                                        61
                                                            61
                                                                              GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
                                       ipkeggvlsfwrgnlanviryfptgalnfafkdkykgiflggvdkhtgfwryfagnlasg 120
                                                                                                                      260;
                                                                                                                                 Similarity
                                                                                                                       Conservative
                                                                                                                                89.2%;
87.2%;
                                                                                                                      Score 1385.5; DB 2
Pred. No. 6.1e-154;
1; Mismatches 16;
                                                                                                                                         22;
                                                                                                                       Indels
                                                                                                                                          Length
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В

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180

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                                                                            expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial porce component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for sevening for agents that alter MPT and/or cell survival. These agents are useful for the prevention or treatment of diseases associated with altered mitochondrial function or dysfunctional cell survival, such as Alzheimer's disease, diabetes
Sequence
                                             mellitus, Parkinson's disease, Huntington's disease, s
mitochondrial encephalopathy, lactic acidosis, stroke,
                                                                                                                                                                                                                                                                          transition (MTP) pore components responsible for mediating transition to the mitochondrial inner membrane. ANT proteins of ADP across the mitochondrial core components e.g. cyclophilins to with other mitochondrial core components e.g. cyclophilins to
                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 2; 186pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polypucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murphy AN,
Velicelebi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-NOV-2000; 2000WO-US30535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human adenine nucleotide translocator-3 (ANT-3) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU01200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU01200 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200
                                                                                                                                                                                                                                                             regulate MPT. The present invention relates to a novel nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MITO-) MITOKOR
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                                                                                                                                                                                                                                                                                                                                present sequence represents human adenine nucleotide translocator-3
P-3) protein. ANT proteins are mitochondrial permeability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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298
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G, Davis RE;
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                                                                 schizophrenia
                                                                                                                                                                                                                                                                                                              transport
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Best Local :
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                                                                                                                                                                   25-APR-2000;
09-JUL-2000;
19-JUL-2000;
                         such
                                                                            Tang
Wang
Zhao
                                                                                                                                                                                                                                                                                           Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                     AAM41427
                                                                                                                (HYSE-)
                                                                                                                                                            03-AUG-2000;
                                                                                                                                                                                               21-JAN-2000;
                                                                                                                                                                                                                 26-DEC-2000;
                                                                                                                                                                                                                                                   WO200153312-A1
                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                 Human polypeptide
                                                                                                                                  29-NOV-2000;
                                                                                                                                                   14-SEP-2000;
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                                                                                                                                         19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 241
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                                                                            QA,
                         as
                                                           2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                              VQGIIIYRAAYEGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPEDTVRRRMMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt gaagatslcfvypldfartrlaadvgksgterefrglgdclvkitksdgirglyggfsvs}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vqgiliyraayfgvydtakgmlpdpknthivvswmlaqtvtavagvvsypfdtvrrrmmm
                        nucleic acids and as central nervous
                                                                                                               HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                            Liu (
Wang :
Zhou
                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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                                                                         , Z,
                                                                                                                                                                                                                 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                               2000US-0488725
                                                                                    Asundi V,
Wehrman T,
                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                             Goodrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.2%;
87.2%;
                        polypeptides, useful system injuries -
                                                                             ₽,
                                                                                                                                                                                                                                                                                                                                                 6358.
                                                                                             Chen
                                                                                   Chen R,
Xu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1385.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NO.
                                                                            Ma Y,
Xue AJ,
nac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.1e-154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22;
                                                                                    Qian XB,
Yang Y,
                                 for
                                treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                    Ren F,
Zhang
                                                                                     J.
                                                                                             Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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6358;

10078pp; English

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AAG36577
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
   25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/Chemokinetic activity, haemostatic and thrombolytic activity, chemotactic/Chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and when the process of the forther activity arthritis and inflammation, leukaemias and when the process of the process of the process of the process of the peripheral networks.
                                                                                                                                                                        06-SEP-2000
                                                                                                                                                                                                                                               Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                    termination sequence
                                                                                                                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 44845.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG36577 standard; Protein; 346 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent \operatorname{did} not form part of the printed specification.
                                                                                                                                   25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                              18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {\tt gaagatslcfvypld} fartrlaadvgksgtere frglgdclvkitksdgirglyggfsvs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260;
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                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                   2000EP-0301439
 99US-0121825.
99US-0123180.
99US-0123548.
99US-0125788.
99US-0126264.
99US-0126785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.2%; Score 1385.5; DB 22; Length 323; 87.2%; Pred. No. 6.8e-154; tive 21; Mismatches 16; Indels 1;
                                                                                                                                                                                                                                                                                                                   pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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            Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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; Pred. No. 7.9e-79;
39; Mismatches 75;
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Arabidopsis thaliana

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AAG36576 standard; Protein; 363 AA

protein fragment SEQ ID NO:

Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;

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Search completed: February 13, 2002, Job time: 108 sec 09:33:11

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062164 mus musculu
091336 rana sylvat
09nhw5 lucilia cup
044093 drosophila
044094 drosophila
025129 halocynthia
062526 drosophila
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Q9i9m9 xenopus lae
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Q9prh2 rana
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rugosa
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| 45                | 44                | 43                 | 42                 | 41                 | 40                 | 39     | 38       | 37                 | 36                 | 35                 | 34                 | ω<br>ω             | 32                 | 31                 | 30                 | 29                | 28                 | 27                 | 26     | 25                 | 24                | 23                | 22                | 21     | 20                |
|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------|--------------------|-------------------|-------------------|-------------------|--------|-------------------|
| 447.5             | 509.5             | 521.5              | 656.5              | 665.5              | 690.5              | 718.5  | 721.5    | 740                | 745                | 746                | 746                | 747                | 749.5              | 750                | 752                | 753               | 753.5              | 755                | 759    | 778                | 819               | 938               | 939               |        | 950.5             |
| 28.9              | 32.9              | 33.7               | 42.4               | 43.0               | 44.6               | 46.4   | 46.6     |                    | 48.2               |                    | 48.2               | 48.3               | 48.4               | 48.5               | 48.6               | 48.7              | 48.7               | 48.8               | 49.1   | 50.3               | 52.9              | 60.6              | 60.7              | 61.4   | 61.4              |
| 158               | 162               | 327                | 262                | 298                | 330                | 305    | 305      | 331                | 307                | 379                | 306                | 388                | 306                | 386                | 307                | 317               | 385                | 303                | 326    | 305                | 170               | 301               | 301               | 307    | 318               |
| 5                 | U                 | 10                 | 10                 | ŋ                  | 10                 | w      | ω        | 10                 | ഗ                  | 10                 | ω                  | 10                 | ഗ                  | 10                 | ر.                 | u                 | 10                 | w                  | ر.     | ω                  | 0                 | տ                 | σ                 | œ      | u                 |
| 076467            | Q26130            | Q9LF44             | Q9AVT6             | Q21809             | Q9FM86             | Q9P875 | Q9P876 , | Q41628             | Q26697             | 049447             | P78754             | 049875             | Q18683             | P93767             | 076286             | Q9N647            | Q9FY52             | 074260             | P91270 | Q9P8M1             | Q9XS69            | Q26006            | Q25692            | Q9XM22 | Q9вJ36            |
| 076467 heterodera | Q26130 plasmodium | Q9lf44 arabidopsis | Q9avt6 picea abies | Q21809 caenorhabdi | Q9fm86 arabidopsis | pichia | pichia   | Q41628 triticum tu | Q26697 trypanosoma | 049447 arabidopsis | P78754 schizosacch | 049875 lupinus alb | Q18683 caenorhabdi | P93767 lycopersico | 076286 trypanosoma | Q9n647 leishmania | Q9fy52 arabidopsis | 074260 candida par | _      | Q9p8ml yarrowia li | Q9xs69 sus scrofa | Q26006 plasmodium | Q25692 plasmodium |        | Q9bj36 toxoplasma |

## ALIGNMENTS

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RESULT

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X MEDLINE—9908342; PubMed—9866197;

X Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

X Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

X Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

X Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

X Y X, and Y in the frog Rana rugosa, inferred from the sec

Y a sex linked gene, App/ATP translocase.";

X Mol. Biol. Evol. 15:1612-1619[1998]

Y -: SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHON

INNER MEMBRANE (BY SIMILARITY).

Y -: SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHON

INNER MEMBRANE (BY SIMILARITY).

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INTEGRAL MEMBRANE (BY SIMILARITY).

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Query Match 93.1
Best Local Similarity 91.1
Matches 273; Conservative
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Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; N
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Score 1446; DB 13;
Pred. No. 1.2e-121;
4; Mismatches 10;
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Best Local
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-!- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FA
EMBL; AB008460; BAA36510.1; -.
EMBL; AB008458; BAA36508.1; -.
EMBL; AB008459; BAA36509.1; -.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
Pfam, PF00153; mito_carr; 3.
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Q9PRH2;
01-MAY-2000
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Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh
Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh
"The origin and differentiation of the heteromorphic s
Z, W, X, and Y in the frog Rana rugosa, inferred from
a sex-linked gene, ADP/ATP translocase.";
Mol. Biol. Evol. 15:1612-1619(1998).

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. M
                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                 PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MTUNCOUPLING.
PROSITE; PS00215; MITOCH_CARRIER; 3.
Inner membrane; Mitochondrion; Transmembrane; Transport.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
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 GAAGATSLCFVYPLDFARTRLAADVGKAGADREFKGLGDCLAKIFRSDGLKGLYQGFNVS
                                                                   IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
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Ranidae; Rana.
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InterPro; IPR002667; Mit_carrier.
InterPro; IPR002067; Mit_uncoupling.
InterPro; IPR0020303; Mit_uncoupling.
Pfam; PF00153; Mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MITOCH_CARRIER: 3.
PROSITE; PS00215; MITOCH_CARRIER: 3.
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01-MAY-1999
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SEQUENCE
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Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
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Mira I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
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Mira I., Ohtani H., Nakamura M., Ichikawa Y., Ichikawa Y., Ichikawa Y., Ichikawa Y., Ichikawa Y., Ichikawa Y., Ichikawa Y., Ichikawa Y., Ichikawa Y., Ichikawa Y., Ichikawa Y., Ichikawa Y., Ichikawa Y., Ichikawa Y., Ichikawa Y., Ichikawa Y., Ichikawa Y., Ichikawa Y., Ichikawa Y., Ichikawa Y., Ichikawa Y., Ichi
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-!- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY EMBL; AB008457; BAA36507.1; -.
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Eukaryota; Metazoa; Chordata;
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Neobatrachia; Ranoidea;
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Last annotation updat
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Pred. No. 5.2e:
L6; Mismatches
    PRT;
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No. 5.2e-121;
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Ranidae; Rana
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p 046373
AC 046373;
TO 01-JUN-1998 (TrEMBLrel. 06, Createw,
DT 01-JUN-1998 (TrEMBLrel. 106, Last sequence upumander)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ADP/ATP TRANSLOCASE.
OS Oryctolagus cuniculus (Rabbit).
Pukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Fukaryota; Metazoa; Lagomorpha; Leporidae; Oryctolagus.
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Best I
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"Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specifi
TDynamic Patterns of Expression During Development.";

L Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHON

C INNER MEMBRANE (BY SIMILARITY).

C-i- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.

R EMBL, AF231347; AAF63471.1; -.

R InterPro; IPR001993; Mitoch_carrier.

R InterPro; IPR002067; Mit_carrier.

R InterPro; IPR002030; Mit_uncoupling.

R PfAm; PF00153; mito_carr; 3.

R PRINTS; PR00926; MITOCHARRIER; 3.

R PROSITE; PR00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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01-OCT-2000
01-JUN-2001
ADENINE NUCL
TISSUE-SKELETAL MUSO
Yamaguchi N., Kasai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271;
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0 (TrEMBLrel. 15, Last
1 (TrEMBLrel. 17, Last
CLEOTIDE TRANSLOCASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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           MUSCLE;
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91.6%;
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ia; Pipoidea; Pipidae;
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.4e-120;
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Matches
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"Expression and seque translocase 1 and 2 g. Submitted (MAR-2000)
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062164;
062164;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ADENINE NUCLEOTIDE CARRIER (ADENINE NUCLEOTIDE TRANSLOCASE 1) (SIMILAR TO SOLUTE CARRIER FAMILY 25 (MITOCHONDRIAL CARRIER, ADENINE NUCLEOTIDE TRANSLOCATOR), MEMBER 4).
                                                               Submitted
-!- SUBCEL
                                                                                                                                                                                                                                                                                                                          STRAIN=BALB/C; TISS Laplace C., Costet
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                             SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                          Submitted
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
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                                                                                                                              SEQUENCE FROM N.A
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mitted (FEB-2001) to the EMBL/Geni
SUBCELLULAR LOCATION: INTEGRAL MI
INNER MEMBRANE (BY SIMILARITY).
SIMILARITY: TO THE MITOCHONDRIAL
L; X74510; CAA52616.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
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Rodentia;
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Pred.
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                      CARRIER
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Best Local S
Matches 266
                                           -!- SUBCELLULAR LOCÁTION: INTEGRAL MEMBRÂNE PROTEIN. MITO
INNER MEMBRANE (BY SIMILARITY).
-!- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
EMBL; U44832; AAA97882.2; -.
R InterPro; IPR001993; Mitoch_carrier.
R InterPro; IPR002067; Mit_carrier.
R Pfam; PF00153; mito_carr; 3.
R PRINTS; PR00926; MITOCH_CARRIER.
R PROSITE; PS00215; MITOCH_CARRIER; 3.
PROSITE; PS00215; MITOCH_CARRIER; 3.
SEQUENCE 317 AA; 35005 MW; SF66B7EDBD5CEB72 CRC64;
.3
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Q91336;
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Cai Q., Greenway S.C., Storey K.B.;
"Differential regulation of the mitochondrial ADP/ATP translocase in wood frogs under freezing stress.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TremBLrel. 01, 01-MAY-1999 (TremBLrel. 10, 01-JUN-2001 (TremBLrel. 17, ADP/ATP TRANSLOCASE.
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PRINTS; PR00926; MITOCARRIER; 3.
PROSITE; PS00215; MITOCH_CARRIER; 3.
Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
SEQUENCE 298 AA; 32904 MW; 3A849FEAB0981462 CRC64;
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EMBL; BC003791; AAH03791.1; -.
EMBL; BC003791; AAH03791.1; -.
MGD; MGI:1353495; Slc25a4.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
                                                                                                                                                                                                                                                                                                                                     Cai Q., Storey K.B.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=LIVER;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rana sylvatica (wood frog).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                         REVISIONS
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cta 1353:69-78(1997).
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Last annotation update)
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Pred. No. 4.9e-119;
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eobatrachia; Ranoidea;
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                                                                      Transport
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Best Local
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Best Local
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Q9NHW5;
01-OCT-2000 (TrEMBLrel. 15, C
01-OCT-2000 (TrEMBLrel. 15, L
01-JUN-2001 (TrEMBLrel. 17, L
ADP/ATP TRANSLOCASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Oestroidea; Calliphoridae; Lucilia.
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lucilia cuprina (Greenbottle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
  129
                                            126
                                                                                                                                                                                                                                                                                                                                                                nner membrane; Mitochondrion; EQUENCE 300 AA; 33036 MW;
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                                                                                 QSGRKGAEIMYSGTIDCWKKIARDEGGRAFFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFK
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TSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGII 185
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245; Conser
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90.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1295;
Pred. No. 4
                                                                                                                                                                                                                                                      Score 1248.5; DB 5
Pred. No. 6.3e-104;
0; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fly)
                                                                                                                                                                                                                                                                                                                                                                Transmembrane; Transport 5459DF0EA0E2E742 CRC64;
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ches 13;
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                                                                                                                                                                                                                                                                                                DB 5;
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RESULT
044094
ID 04
AC 04
DT 01
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Best Local :
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01-JUN-1998
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila pseudoobscura (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muso: Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INNER MEMBRANE (BY SIMILARITY).
-!- SIMILARITY: TO THE MITOCHONDRIAL
EMBL; AF025798; AAB87883.1; -.
F1yBase: FBgn0023292; Dpse\sesB.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
Genetica 0:0-0(1997).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
   044094;
01-JUN-1998
                           044094
                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
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                                                                                      ALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVRIPKE
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                                                                                                                                                                                                                                                                                      AIGFVKDFAAGGISAAVSKTAVAPIERVKLLLQVQHISKQISPDKQYKGMVDCFIRIPKE
                                                                                                                                                                                                                                                                                                                                                                                                   membrane; Mitochondrion; ER 288 288 NA; 31725 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TremBLrel. 06, Created)
(TremBLrel. 06, Last sequence up)
(TremBLrel. 17, Last annotation
                                                                                                                                                                                                                                                                                                                                       Conservative
   (TrEMBLrel.
                            PRELIMINARY;
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80.4%;
   , 30
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   Created)
                                                                                                                                                                                                                                                                                                                                  Score 1190.5; DB 5; Pred. No. 9.4e-99; "" matches 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARRIER FAMILY.
                            288
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Best Local Sin
Matches 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INNER MEMBRANE (BY SIMILARITY).
-!- SIMILARITY: TO THE MITOCHONDRIAL CA
EMBL; AF025799; AAB87884.1; --
F1yBase; FBgn0023237; Dsub\sesB.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSTTE; PS00215; MITOCARRIER.
PROSTTE; PS00215; MITOCARRIER.
ORN.TER
288
889
SEQUENCE 288 AA; 31775 MW; 06A1D1E4
                                                                                                                                    Q25129 PRELIMINARY; PRT; 304 AA. Q25129; O1-NOV-1996 (TrEMBLrel. 01, Created) O1-NOV-1996 (TrEMBLrel. 01, Last sequence update) O1-JUN-2001 (TrEMBLrel. 17, Last annotation updat ADT/ATP TRANSLOCASE. HRATL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zeng L.-W:, Comeron J.M., Chen B., Kreitman M.;
Genetica 0:0-0(1997).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila subobscura (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                Halocynthia roretzi (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata;
Stolidobranchia; Pyuridae; Halocynthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ephydroidea; Dro
NCBI_TaxID=7241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
ADP/ATP TRANSLOCASE (FRAGMENT).
 SEQUENCE FROM N.A.
Miya T., Makabe K.,
                                        Submitted
                                                                                     Stolidobranchia;
NCBI_TaxID=7729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                             SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                     IIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMMOSGR 244
                                                                                                                                                                                                                                                                                                                                                                                      ATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGI
                                                                                                                                                                                                                                                                                                                                                                                                                                       QEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMGFVKDFAAGGISAAVSKTAVAPIERVKLLLQVQHISKQISPDKQYKGMVDCFIRIPKE 66
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A Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
B Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Wan K.H., Doyle C., Baxter E.G., Helt G., Refankoch C., Baldwin D.,
Ballew R.M., Baylayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
A Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
A Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
A Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
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PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Musc Ephydroidea; Drosophilidae; Drosophila.
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-!- SIMILARITY: TO THE MITOCHONDRIAL
EMBL; D83059; BAA11765.1; -.
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
INNER MEMBRANE (BY SIMILARITY).
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1; Mismatches 50;
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D6B654880 CRC64;
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RESULT Q9H0C2 ID Q9 AC Q9 DT 01 DT 01 DT 01

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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Klimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reesee M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yeb J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
RT Trie genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 215; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-OREGON-R;
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InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCH_CARRIER; UNKNOWN_2.
SEQUENCE 307 AA; 33744 MW; 3D6B3DFD82061COC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhang Y.Q., Davis A.W., Root
Submitted (MAY-1998) to the
EMBL; AE003484; AAF47956.1;
EMBL; Y10618; CAA71629.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dodson K., D
Durbin K.J.,
256
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                   TDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
                                                                                                                                           VLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGAT 126
                                                                                                                                                                                                                                                                                                                 SFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVRIPKEQE 66
                                                                                          YRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRWMWQSGRKG
SEMVYKNTAHCWLVIAKQEGIGAFFKGALSNIIRGTGGALVLALYDEMKKY
                                                                       YRAAYFGFYDTCRDFLPNPKSTPFYVSWAIAQVVTTVAGIASYPFDTVRRRMMMQSGLKK
                                                                                                                                                                                                                        FSSFWRGNLANVIRYFPTQALNFAFKDVYKSVFLGGVDKHKQFWRHFAGNLASGGAAGAT
                                                                                                                                                                                                                                                                                                SFLMDFMMGGVSAAIAKTAVAPIERVKLILQVQEVSKQIAADQRYKGIVDCFIRIPKEQG 76
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73.9%;
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sta C.C., Ferraz C., Ferriera S.
A.E., Garg N.S., Gelbart W.M.,
Gu Z., Guan P., Har
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roote J., Ashburner M.;
                                                                                                                                                                                                                                                                                                                                                                       27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                       Score 1125.5;
Pred. No. 6.9
                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       .5; DB 5;
i.9e-93;
                                                                                                                                                                                                                                                                                                                                                                         48;
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                                    297
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Best Local Sin
Matches 210;
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-i-SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCI
INNER MEMBRANE (BY SIMILARITY).
-i-SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
-i-SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
EMBL; AL136857; CAB66791.1; -
InterPro: IPR001993; Mitoch_carrier.
InterPro: IPR002067; Mitoch_carrier.
InterPro: PR002067; Mitoch_carrier.
PF6am; PF00153; mitoch_carrier.
PF6am; PF00153; mitoch_carrier.
PROSITE; PR000205; MITOCH_CARRIER.
PROSITE; PR000205; MITOCH_CARRIER; 1.
                                                                                                                                                                                               045865;
045865;
01-JUN-1998
01-JUN-1998
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLING=94150718; PubMed=7906398;
MIlson R., Ainscough R., Anderson K., Baynes C.
Bonfield J., Burton J., Connell M., Copsey T.,
Bonfield J., Burton J., Connell R., Favello
                                                                                                                      Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                      Lloyd
                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Inner membrane; Mitochondrion; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-TESTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                            --AKRQYKGTLDCFVKIYQHEGISSFFRGAFSNVLRGTGGALVLVLYDKIKEF
                                                                                                                                                                                                                                                                                                                                                       QEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVRIPKE
                                                                                                                                                                                                                                                                                                                         KGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
                                                                                                                                                                                                                                                                                                                                                                                                         ATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGFFSFWRGNLANVIRYFPTQALNFAFKDKYKQLFMSGVNKEKQFWRWFLANLASGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASSFGKDLLAGGVAAAVSKTAVAPIERVKLLLQVQASSKQISPEARYKGMVDCLVRIPRE
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                                                                         (NOV-1996)
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3 (TrEMBLrel.
1 (TrEMBLrel.
                                                                                                                                                                                                                                                PRELIMINARY;
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Primates;
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71.7%;
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                                                                           the
                                                                                                                                     oda; Chromadorea; Rhabditida;
Caenorhabditis.
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                                                                           EMBL/GenBank/DDBJ
                                                                                                                                                                                               Created)
Last sequence update)
Last annotation updat
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Pred. No. 9
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 s C., Berner J., (T., Cooper J., (Fulton
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                          Berks M.,
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                                                                                                                                                  Rhabditoidea;
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                Coulson
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RESULT
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Best Local :
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InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PR0051TE; PS00215; MITOCARRIER; 3.
Inner membrane; Mitochondrion; Repeat;
SEQUENCE 300 AA; 33044 MW; 8E50F7D
                                                                                                                                                                                                                                                                                                                                              P91410
P91410;
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Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton Gardner A., Green P., Hawkins T., Hillier L., Jier M., Joh Jones M., Kershaw J., Kirsten J., Laister N., Latrellle P. Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Calla Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.
                                                                                                                                                                                                                                                                             01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
SIMILAR TO ADP/ATP TRANSLOCASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INNER MEMBRANE (BY SIMILARITY).
-i- SIMILARITY: TO THE MITOCHONDRIAL CARRIER
EMBL; 282059; CAB04874.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 368:32-38(1994).
                                                                                                                                                                                             Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                               Caenorhabditis elegans.
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                                                                                                                                  MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                   STRAIN-BRISTOL
                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAAYFGIYDTAKGML-PDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRWMMQSGRKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LCFVYPLDFARTRLAADIGKAN-DREFKGLADCLIKIVKSDGPIGLYRGFFVSVQGIIIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AALWRGNLANVIRYFPTQAMNFAFKDTYKAIFLEGLDKKKDFWKFFAGNLASGGAAGATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203;
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                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%;
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Pred. No. 1.6e
34; Mismatches
                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                 O'Callaghan
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                    Shownkeen
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Geisel C., Stellyes L.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
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| ressed at the m ACROSS THE . MITOCHONDRIAL . R FAMILY.  | Chen S.T.<br>Tier which   | TRANSLOCASE Euteleostomi, Homo. R., Wurzel c   |   | Q9z2b2<br>P16261<br>Q21153<br>Q21153<br>Q2558<br>Q95258<br>P16260<br>Q9ujs0<br>Q9ujs0<br>Q9ujs0<br>Q9ujs0<br>Q9ujs3<br>Q9x3x2<br>Q9x3x3<br>Q9x3x3<br>Q9x3x3<br>Q9x3x3<br>Q9x3x3 |
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01-FEB-1995 (Rel. 31, Created)

01-FEB-1995 (Rel. 31, Last sequence update)

20-AUG-2001 (Rel. 40, Last annotation update)

ADP,ATP CARRIER PROTEIN, FIBROBLAST ISOFORM (/
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PRINTS; PR00926; MITOCARRIER;
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PROSITE; PS00215; MITOCH_CARRIER;
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-!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS
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PRINTS: PR00927; ADPTRNSLCASE.
PROSITE; PS00215; MITOCH_CARRIER;
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Shinohara Y., Kamida M., Yamazaki
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INNER MEMBRANE
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                                                                                         GAAGATSLCFYYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                                                                                                MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYT
                                      VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMM
                                                                            GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFKGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                                 IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
                                                                                                                                            IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
                                                                                                                                                                                   MTDAAVSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
                         VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIFISWMIAQSVTAVAGLTSYPFDTVRRRMMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00153;
                                                                                                                                                                                                                                    Similarity 98.:
93; Conservative
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IPR001993; Mitoch_carrier.
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32901 MW;
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Pred. No. 1.1e
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ns as long as its content is in
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                                                                                                                                                                                                                                                  .1e-128;
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EMBL; U10404; AAA19009.1; -.
EMBL; W70847; CAA50196.1; -.
EMBL; W70847; CAA50196.1; -.
InterPro; IPR002607; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR00153; Mitoch_carr; 3.
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or send a
                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADT2_MOUSE STANDARD; PRT; 2
P51881; Q61311;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
ADP,ATP CARRIER PROTEIN, FIBROBLAST IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97059403; PubMed-8903724; Ellison J.W., Li X., Francke U., "Rapid evolution of human pseudoa
                                                                PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00927; ADPTRNSLCASE.
PROSITE; PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                              Laplace C.;
Submitted (FEB-1997) to
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STRAIN-C57BL/6; TISSUE-Brain;
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Eukaryota; Metazoa;
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                    TRANSMEM
                                       TRANSMEM
                                                Multigene
                                                        Mitochondrion;
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                                                                                                                                                                                                                                              DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY
                                                                                                                                                                                                                                                                                   MITOCHONDRIAL INNER SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                      FUNCTION: CATALYZES
                                                                                                                                                                                                                                                                INNER MEMBRANE
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e family.
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Rodentia;
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EXCHANGE OF ADP A
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Sciurognathi; Muridae;
(POTENTIAL).
(POTENTIAL).
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                                                       Transmembrane;
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AND ATP ACROSS
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Best Local Sin
Matches 292;
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SEQUENCE
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REPEAT
         EMBL; M24103; AAA30769.1; PIR; B43646; B43646.
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ADT3_BOVIN
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                                                                                                              DOMAIN: COMPOSED OF SIMILARITY: BELONGS
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92; Conservative
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Mit_carrier
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01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ADP,ATP CARRIER PROTEIN, ISOFORM T2 (ADP/ATP,
NUCLEOTIDE TRANSLOCATOR 3) (ANT 3).
SLC25A6 OR ANT3.
Bos tannotation
                                                                                                                                                                                                                                                                                                                    Powell S.J., Medd S.M., Runswick M.J., Walker J
"Two bovine genes for mitochondrial ADP/ATP tran
differences in various tissues.";
Biochemistry 28:866-873(1989).
-i- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND
use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Peo
                                                                                           European Bioinformatics Institute.
                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - EDUTOPEAN HOLOGOMETRICS INSTITUTE. There are no restrictions on its by non-profit institutions as long as its content is in no way
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Pred. No. 3.8e
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Best Local Sin
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PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00927; ADPTRNSLCASE.
PROSTITE; PS00215; MITOCH_CARRIER;
Mitochondrion; Inner mamballitare.
Multiface.
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REPEAT
SEQUENCE
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TRANSMEM
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TRANSMEM
Houldsworth J., Attarui G., ATTAM distinct genes for ADP/ATP translocase are level in adult human liver."; 45:377-381(1988).
                                                                                   Cozens A.L., Runswick M.J., Walker J. "DNA sequences of two expressed nucle ADP/ATP translocase.";
                                                                                                          SEQUENCE FROM N.A. MEDLINE=89236396; PubMed=2541251;
                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                        01-OCT-1989 (Rel. 12, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP
                                                                                                                                                                                                                                        ADT3
                                                                                                                                                                                                                                                HUMAN
                                                                                 ADP/ATP
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                                     MEDLINE=88124845;
                                              TISSUE=Liver;
                                                       SEQUENCE OF
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PF00153; mito_carr: 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitochondrion; In Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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InterPro; IPR001993; Mitoch_carrier.
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-!- SIMILARITY: BELONGS TO THE MITOCHONDI
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- I- SUBUNIT: HOMODIMER.
- I- SUBCELLULAR LOCATION: INTEGRAL MEMBR
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B28116; B28116.
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Pred. No. 2.3e
13; Mismatches
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InterPro;
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Biochim. Biophys. Acta 1152:192-196(1993).
-i- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER;
PRINTS; PR00927; ADPTRNSLCASE.
PROSITE; PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-SPRAGUE-DAWLEY, AND WISTAR; TISSUE-Heart, MEDLINE-94002161; PubMed-8399300; Shinohara Y., Kamida M., Yamazaki N., Terada H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X61667; CAA43842.1; - EMBL; D12770; BAA02237.1; -
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Mammalia; Eutheria; Rodentia;
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ADP,ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP
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mes 266; Conservative
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SUBUNIT: HOMODIMER.
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VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMM
                                                                                                      IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASG
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EMBL; M24102; AAA30768.1; -.
PIR; A03181; XWBO.
PIR; A24822; A24822.
PIR; A43646; A43646.
InterPro; IPR0012067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs an unusually short 3'-noncoding sequence.",
Biochem. Biophys. Res. Commun. 138:850-857(1986).
-!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Powell S.J., Medd S.M., Runswick M.J., "Two bovine genes for mitochondrial ADI differences in various tissues."; Biochemistry 28:866-873(1989).
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20-AUG-2001 (Rel. 40, Last annotation update)
ADP_ATP CARRIER PROTEIN, HEART ISOFORM T1 (ADP/ATP
(ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).
                                              PRINTS; PR00926; MITOCARRIER. PRINTS; PR00927; ADPTRNSLCASE. PROSITE; PS00215; MITOCH_CARRIER;
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Hoppe-Seyler's Z.
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MEDLINE-89229093; PubMed-2540808;
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NCBI_TaxID=9913;
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  Multigene family; Methylation
                       Mitochondrion;
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                       membrane;
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01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 16, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ADP,ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).
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Li K., Warner C.K.,
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Mammalia; Eutheria; Primates;
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                                           human muscle adenine nucleotide translocator gene has four exons, biol. Chem. 264:1398-14004(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVRI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGATSLCFVYPLDFARTRLAADVGKGAAQREFTGLGNCITKIFKSDGLRGLYQGFNVSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASGG
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                                                                                                                                                                                               N.A.
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   PubMed=2823266; K., Wade R.P.,
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Pred. No. 8
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Catarrhini; Hominidae;
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(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of a leader peptide, divergence from a fibroblast translocator cDNA, and coevolution with mitochondrial DNA genes."; Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).
                                                                                                                                                                                                                                                                                                                                       Mitochondrion;
                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00927; PROSITE; PS00215;
                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00153; mito_carr; 3. PRINTS; PR00926; MITOCARRIER.
                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "CDNA sequence of a human skeletal muscle ADP/ATP translocator: of a leader peptide, divergence from a fibroblast translocator of
                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                  REPEAT
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            121
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; A39891;
; S03893;
; A44778;
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SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C. Natl. Acad. Sci. U.S.A. 85:377-381(1988) FUNCTION: CATALYZES THE EXCHANGE OF ADP AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MITOCHONDRIAL INNER MEMBRANE. SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                  103220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         distinct genes for ADP/ATP translocase
           GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
                                                                             MGDHAWSFLKDFLAGGVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in adult human liver.
Natl. Acad. Sci. U.S.
                                                                                                                                                                                                                                                                                                                                                PR00927; ADPTRNSLCASE.; PS00215; MITOCH_CARRIER;
                                                                                                                                                                              227
298
                                                                                                                         Conservative
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A44778.
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A39891.
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33064
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                                                                                                                                   91.3%;
89.2%;
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3.
G -> A (IN REF.
KGA -> RR (IN REF.
V -> L (IN REF. 3)
WW; 59F0DFAEC4E7CFBB CRC64;
DB 1; Leng
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                                                                                                                        Score 1413; I
Pred. No. 1.1e
.6; Mismatches
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Transmembrane; Transport;
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RIAL CARRIER FAMILY
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16;
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                                                                                                                                             Length 298;
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TRANSMEM
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p48962;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ADP.ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).
                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a copyright the EWISS Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE-Brain;
MEDLINE-97059403; PubMed-8903724;
Ellison J.W., Li X., Francke U., Shapiro I
"Rapid evolution of human pseudoautosomal
                                                                                                                                                                                                                                                                    Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER;
PRINTS; PR00927; ADPTHNSLCASE.
PROSITE; PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                   EMBL; U27315; AAC52837.1; --
MGD; MGI:1353495; S1c25a4.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mamm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
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                                                                                                                                                                                                                                    Multigene family.
                                                                                                                                                                                                                                                        Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: CATALYZES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLC25A4 OR ANT1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYD3IKKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAGATSLCFVYPLDFARTRLAADVGKGAAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome 7:25-30(1996).
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91
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208
32870
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Rodentia;
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(POTENTIAL).
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No. 1
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                                                                                                                                                                                                                                                      Transmembrane;
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   DB 1;
.6e-118;
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                                                                    CRC64;
                   Length 298;
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RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RY MEDLINE=20196006; PubMed=10731132;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne ...

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Pfeiffer B.D.,

RA George R.A., Lewis S.E., Yandell M.D., Zhang O., Chen L.X.,

RA George R.A., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

"""koya D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

""" koya D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

""" koya D., Botchan M.R., Bouck J., Brokstein P., Center A., Chandra I.,
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PRT;

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Q26365; Q26254; P91614; Q9V270;

15-JUL-1998 (Rel. 36, Last sequence update)

15-JUL-1998 (Rel. 40, Last annotation update)

20-AUG-2001 (Rel. 40, Last annotation update)

ADP, ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE)
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J. Mol. Evol. 35:44-50(1992)
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Pterygota; Neoptera; Endopterygota; Diptera; Brachyc
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                  "Molecular analysis of a candidate isolation between sibling species caperientia 50:749-762(1994).
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Hutter P., Karch F.;
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EMBL/GenBank/DDBJ databases.
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FA HOSELIA D., HOUSEON K.A., HOWLANDER, J., Wei M.-H., IDEGWAM C.,
FA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
FA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
FA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
FA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
FA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
FA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
FA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
FA Lasko P., Lei Y., Mobarry C., Morris J., Moshrefi A.,
FA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
FA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
FA Merkulov G., Milshina N.V., Molary C., Morris J., Moshrefi A.,
FA Meston D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
FA RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
FA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
FA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
FA Syliskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
FA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
FA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
FA Yebn S.M., Myers E.W., Rubin G.M., Venter E., Yang S., Yao Q.A.,
FA Yebn S.A., Myers E.W., Rubin G.M., Venter J.C.,
FA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
FA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
FA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
FA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
FA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
FA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
FA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
FA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
FA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
FA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
FA Gibbs R.A., Myers E.W., Rubin G.M., Venter B., Jano Q., Jano Q.,
FA Gibbs R.A., Myers E.W., Rubin G.M., Venter B.,
FA Gibbs R.A., Myers 
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                                                                                                                                                                                                                                                                                                                                                                                                                FlyBase; FBgn0003360; sesB.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Delcher A., Deng Z., Mays A.D., Dew I., Dietz S
up L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
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G -> A (IN REF. 2).
Score 1218.5;
Pred. No. 2.2e
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Q27238;
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"A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Cul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ADP,ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE)
                                                                                          Pfam; PF00153; mito_carr; 3. PRINTS; PR00926; MITOCARRIER.
                                                                                                                       InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier
                                                                                                                                                   EMBL; L11618; AAB04104.
EMBL; L11617; AAB04105.
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                                                                                                                                                                                                                                              between the Swiss Institute of Bioinf
the European Bioinformatics Institute.
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                                                     Mitochondrion;
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                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: HOMODIMER (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION:
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                                                                                                                                                                                                                                  non-profit
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SEQUENCE
                                                                                                                                                                                                           the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glyceraldehyde-3-phosphate dehydrogenase
J. Biol. Chem. 266:24044-24047(1991).
-!- FUNCTION: CATALYZES THE EXCHANGE OF I
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01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ADP,ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE)
  Pfam; PF00153; mito_carr; 3. PRINTS; PR00926; MITOCARRIER PRINTS; PR00927; ADPTRNSLCAS; PROSITE; PS00215; MITOCH_CAR
                                                                                          PIR; A41677; A41677.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is between the Swiss Institute of Bioinformation
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Eukaryota; Viridiplantae;
                                                                                                                                                                  EMBL; M76669; AAA33027.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92084708; PubMed=1748677;
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SUBUNIT: HOMODIMER (BY SIMILARITY)
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RESULT
ADT1_GO:
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Best I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mitochondrion;
TRANSMEM 45
TRANSMEM 108
TRANSMEM 151
TRANSMEM 209
TRANSMEM 248
TRANSMEM 304
SEQUENCE 339
                                                      between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i modified and this statement is not removed. Us entities requires a license agreement (See http or send an email to license@isb-sib.ch).
                                                                                                                                                                                                  Shin H., Brown R.M. Jr.; "Two cDNA sequences for the adenine nucleotide tr CANT2, from cotton fibers (Gossypium hirsutum).";
                                                                                                                                                                                                                                                                                                                                             15-JUL 1998 (Rel. 36, Created)
15-JUL 1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ADP,ATP CARRIER PROTEIN 1, MITOCHONDRIAL PRECURSOR
TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                    _GOSHI
                                                                                                                              This
                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                            ADT1_GOSHI
O22342;
                                                                                                                                                                                       (In)
                                                                                                                                                                                                                                       STRAIN-CV.
                                                                                                                                                                                                                                                                                                                         Gossypium hirsutum
                     InterPro;
                                EMBL; AF006489; AAB72047.1;
                                                                                                                                                                                                                                                                         NCBI_TaxID=3635;
                                                                                                                                                                                                                                                                                                                                       ANT1.
                                                                                                                                                     - I - SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243
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                                                                                                                                                                                                                                                     EQUENCE FROM N.A.
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                                                                                                                                                                            ) Plant Gene Register PGR97-130.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                  INNER MEMBRANE (BY SIMILARITY)
                                                                                                                              SWISS-PROT entry is copyright. It is produced through a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATSLCFVYPLDFARTRLAADVGKAGAEREERGLGDCLVKIYKSDGIKGLYQGFNVSVQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADK--QYKGIIDCVVRIPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IIIYRAAYFGIYDTAKGML-PDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMMQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAFVKDLLAGGTAGAISKTAVAPIERVKLLLQTQDSNPMIKSGQVPRYTGIVNCFVRVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IIVYRGAYFGLYDTAKGVLFKDERTANFFAKWAVAQAVTAGAGVLSYPFDTVRRRLMMQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGSLLIVYPLDFARTRLAADVG-SGKSREFTGLVDCLSKVVKRGGPMALYQGFGVSVQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQGVASFWRGNLANVVRYFPTQAFNFAFKDTIKGLF-PKYSPKTDFWRFFVVNLASGGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
       IPR002067; Mit_carrier.
IPR001993; Mitoch_carrier
                                                                                                                                                                                                                                       TEXAS
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                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                      MARKER 1; TISSUE-Fiber;
                                                                                                                                                                                                                                                                                                                           (Upland
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65.8%;
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                                                                                                                                                                                                                                                                                                                           cotton)
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Pred. No. 5.4e
29; Mismatches
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3 (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
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(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       968; DB 1;
No. 5.4e-79;
                                                                                                                                                                                                              nucleotide translocator,
                                                                                                                                                                                                                                                                                                                                                                                                                          386
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                                                                                        There are no rest
                                                                    http://www.isb-sib
                                                                               Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64;
                                                                                                                  and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 339
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                                                                               ьy
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                                                                                                      restrictions
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                                                                                                                   EMBL
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                                                                                                                  collaboration
                                                                                                                                                                                                                 CANT1
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                                                                    .ch/announce/
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                                                                                commercial
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Best Local S
Matches 169
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TRANSIT 1 76
CHAIN 77 386
TRANSMEM 90 107
TRANSMEM 152 170
TRANSMEM 155 212
TRANSMEM 195 215
TRANSMEM 256 275
                                                                                                                                                                                                                                                               ADT_SCHPO
Q09188;
Q1-NOV-1997
                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ADP,ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE)
TRANSLOCATOR) (ANT).
ANCI OR SPBC530.10C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
TRANSMEM
                                                        "Cloning of the gene encoding the mitochondrial adenine nucleotide carrier of Schizosaccharomyces pombe by functional complementation Saccharomyces cerevisiae.";
    Lyne
                 SEQUENCE FROM N.A. STRAIN=972;
                                                 Saccharomyces cerevisiae. Gene 171:113-117(1996).
                                                                                         MEDLINE-96257204; PubMed-8675018; Couzin N., Trezeguet V., Saux A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00927; ADPTRNSLCASE.
PROSITE; PS00215; MITOCH_CARRIER;
                                                                                                                    STRAIN=972;
                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                              Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                   NCBI_TaxID=4896
                                                                                                                                                               Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                             377
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                                                                                                                                                                                                                                                                                                                                                                                                                                             IIIYRAAYFGIYDTAK-----GMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGA 125
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                                                                                                                                                                                                                                                                                                                                                                   --KKY
                                                                                                                                                                                                                                                                                                                                                                                                                                  IIVYRGLYFGMYDSLKPVLLTGSMQDSFFASFVLGWLI----TNGAALASYPIDTVRRRM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSLCFVYPLDFARTRLAAD--VGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GFGSLWRGNTANVIRYFPTQALNFAFKDYFKRLFNFKKD-RDGYWKWFAGNLASGGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQ-HASKQITADKQYKGIIDCVVRIPKEQ
                                                                                                                                                                                                                                                                                                                                                                                      MMTSGKA---VKYKSSLDAFSQILKNEGGKSLFKGAGSNILRAIAGAGVLAGYDKLQLIV
                                                                                                                                                                                                                                                                                                                                                                                                           MMQSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEİ----
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     Wood V.,
                                                                                                                                                                                                                                                                                                                                             381
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                                                                                                                                                                                                                                                                                      STANDARD;
      Rajandream
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    M.A.,
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Pred. No. 2
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      Barrell
                                                                                                                                                                                                                                                                                     322
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.2e-61;
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     В
     .G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 386;
     Rieger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                       376
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RESULT 15
ADT_CHLRE
ID ADT_CHLRE
ACC P2708
DT 01-AU
DT 01-AU
DT 01-OC
DE ADP,A
DE TRANS
GN ABT.
OS Chlam
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                                                      ADT_CHLRE STANDARD; PRT; 3 P27080; P27080; O1-AUG-1992 (Rel. 23, Created) O1-AUG-1992 (Rel. 23, Last sequence up O1-OCT-1994 (Rel. 30, Last annotation ADP, ATP CARRIER PROTEIN (ADP/ATP TRANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z49974; CAA90275.1; -.
EMBL; AL023634; CAA19176.1; -.
HSSP; P04002; lATF
InterPro; IPR002067; Mit_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
-- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
Chlamydomonas reinhardtı. Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00153; mito_carr; 3, PRINTS; PR00926; MITOCARRIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                            TRANSLOCATOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00927; ADPTRNSLCASE. PROSITE; PS00215; MITOCH_CARRIER;
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    -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
    -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

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                                                                                                                                                                                                                           QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIK 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sharpe J.A., Day A.; "Structure, evolution and expression of the mitochondrial ADP/ATP translocator gene from Chlamydomonas reinhardtii.";
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pRINTS; PR00926; MITO_CARRIER:
PRINTS; PR00927; ADPTRUSLCASE.
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-I- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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Mol. Gen. Genet. 237:134-144(1993).
-i- FUNCTION: CATALYZES THE EXCHANGE OF
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NCBI_TaxID=3055;
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9; Mismatches 78
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## ALIGNMENTS

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A;Cross-references: GDB:125190; OMIM:300150

A;Map position: Xq13-Xq26
A;Map position: Xq13-Xq26
A;Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein r;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                      Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Battini, R.; Ferrari, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R. J. Biol. Chem. 262, 4355-4359, 1987
A;Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regu A;Reference number: A29132; MUID:87166056
A;Accession: A29132
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C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: A29132; C28116
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A;Residues: 47-65,'G',67-110,'L',112-161,'G',163-298 <HOU>
A;Cross-references: GB:J03591; NID:g339720; PIDN:AAA36749.1;
A;Experimental source: clone pHAT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-298 <BAT>
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Best Local Similarity 100.
Matches 298; Conservative
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61
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                                                                                                     MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
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A;Cross-references: EMBL:X70847
A;Cross-references: EMBL:X70847
A;Cross-references: EMBL:X70847
C;Superfamily: ADP,ATP carrier protein: C;Keywords: duplication; transmembrane protein
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP3>F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3-P
A;Cross-references: GB:M24103; NID:g529416; PIDN:AAA30769.1; PID:g529417 C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat h C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein
                                                                                                                                                                        Biochemistry 28, 866-873, 1989
A; Title: Two bovine genes for mitochondrial
A; Reference number: A43646; MUID:89229093
A; Accession: B43646
                                                                                                                                                                                                                                                                                                                  ADP,ATP carrier protein T2 - bovine C;Species: Bos primigenius taurus (cattle) C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change C;Accession: B43646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
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                                                                            A; Molecule type: mRNA
A; Residues: 1-298 < POW>
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A; Residues: 1-298 <COS>
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Matches

Conservative

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Mismatches

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A;Cross references; GDB:125184; OMIM:300151; OMIM:403000
A;Cross references; GDB:125184; OMIM:300151; OMIM:403000
A;Map position: Xp22.32 - Xp22.32; Yp11.3 - Yp11.3
A;Note: there may be some confusion in the assignment of sequences for GDB:ANT2
C;Superfamily; ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F;2-298/Product: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                               R;Houldsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A;Title: Two distinct genes for ADP/ATP translocase
A;Reference number: A94197; MUID:88124845
A;Accession: B28116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: DNA sequences of two expressed nuclear genes A;Reference number: S03893; MUID:89236396 A;Accession: S03894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000
C;Accession: S03894; B28116
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                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 36-104,'R',106,'A',109-298 <HOU>
A;Cross-references: GB:J03592; NID:g339722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-298 <COZ>
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94.0%;
92.6%;
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Score 1454;
Pred. No. 3
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Pred. No. 1
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  .4e-121;
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F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>F;2/Modified site: acetylated amino end (Ser) (in mature form) #F;52/Modified site: N6-methyllysine (Lys) #status predicted

#status

experimental

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W. Alternate hames: ADP/ATP translocase T1

C. Species: Bos primigenius taurus (cattle)
C. Species: Bos primigenius taurus (cattle)
C. Species: A05646; AZ4822; ADJ81; AGJ33; S95369
R. Povell. 1. S.J.; Medd. S.M.; Runswick, M.J.; Walker, J.E.
Blochemistry 28, 866-873, 1999
A. Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed di
A. Residues: 1-298 FOPW
A. Cross references: GB:M2102; NID:S229414; PIDN:AAA30768.1; PID:g529415
A. Residues: 1-298 FOPW
A. Residues: 1-298 FOPW
A. Residues: 1-298 FOPW
A. Reference number: A24822; MUID:8529416; PIDN:AAA30768.1; PID:g529415
A. Residues: 1-298 FOPW
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RESULT
S37210
ADP, ATP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: adenine nucleotide C;Species: Mus musculus (house mouse) C;Date: 06-Jan-1995 #sequence_revision C;Accession: S37210
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A; Residues: 1-298 <LAP>
A; Cross-references: EMBL: X74510;
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             VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMM
                                                                   GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS 180
                                                                                                           MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR 60
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                                                    GAAGATSLCFVYPLDFARTRLAADVGKGSSQREFNGLGDCLTKIFKSDGLKGLYQGFSVS
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266; Conser
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267; Conserv
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                                                                                                                                                                                                                      Score 1417; D
Pred. No. 6.5e
15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           NID: g402627; PIDN: CAA52616.1;
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Pred. No. 4.3e-118;
6; Mismatches 14;
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No. 6.
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les 16;
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C:Species: Homo sapiens (man)
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: A44778; S03893; A39891; A28116
R;Li, K; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R., J. Biol. Chem. 264, 13998-14004, 1989
J. Biol. Chem. 264, 13998-14004, 1989
A;Title: A human muscle adenine nucleotice translocator gene has four exons.
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R;Shinohara, Y.; Kamida, M.; Yamazaki, N.;
Biochim. Biophys. Acta 1152, 192-196, 1993
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C;Date: 02-Aug-1996 #sequence_revision 02-
C;Accession: I60173
R;Shinoharr
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C; Keywords: du
                                                                       A; Residues: 1-298 <LIA>
                                                                                                  A; Molecule type: DNA
                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                        N; Alternate names: mitochondrial ADP, ATP translocase
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADP, ATP carrier protein T1 - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-298 < RES>
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;Cross-references: GB:J04982; NID:g178658; ;Cozens, A.L.; Runswick, M.J.; Walker, J.E
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Best Local :
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ily: ADP,ATP carrier protein; ADP,ATP carrier
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Pred. No. 6.
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                                           PIDN: AAA51736.1;
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5.5e-118;
nes 15;
                                                                                                                                                                                                                                                                               Kudoh, J.; Fukuyama, R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 298;
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                                                                                                                                                                                                                           located
            submitted to the EMBL Data Library, February 1993 A;Description: A cDNA encoding an ADP/ATP carrier A;Reference number: S31935
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                                                                                                                                                                                                                     ADP, ATP carrier
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89.2%;
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A; Map position: 4q35-4q35
C; Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology C; Keywords: duplication; homodimer; mitochondrion; transmembrane protein F; 2-298/Product: ADP, ATP carrier protein #status predicted <AAT>
F; 5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>
F; 110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>
F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>
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Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A;Title: Two distinct genes for ADP/ATP translocase
A;Reference number: A94197; MUID:88124845
A;Accession: A28116...
C;Species: Anopheles gambiae (African malaria mosquito)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C;Accession: S31935; S31936
C;Accession: S31935; S31936
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A;Residues: 1-37 <HOU>
A;Cross-references: GB:J03593; NID:g339724; PIDN:AAA36751.1; PID:g339725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA A;Residues: 1-15,'A',17-146,'RR',149,151-226,'L',228-298 <NEC> A;Cross references: GB:J02966; NID:9339919; PIDN:AAA61223.1; PID:9339920 A;Experimental source: clone_pHMANT
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A;Title: cDNA sequence of a human skeletal muscle
A;Reference number: A39891; MUID:88041149
A;Accession: A39891
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A;Accession: S03893
A;Status: not compared with conceptual translation
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A; Title: DNA sequences of two expressed nuclear genes A; Reference number: S03893; MUID:89236396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: GDB:ANT1; T1
A;Cross-references: GDB:119680; OMIM:103220
                                                                                                                                                                                                                                                                                         QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQTTADKQYKGIIDCVVR
                                                                                                                                                                                                                                                                                                                                                                                                        VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                                                                                                                                                            QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
                                                                                                                                                                                                                                                                                                                                                                           VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLVSYPFDTVRRRMMM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGDHAWSFLKDFLAGGVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                                                                                               protein - African malaria mosquito
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Pred. No. 1
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les 16;
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                                                             10-Sep-1999
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from

the mosquito Anopheles gambiae

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A;Accession: S31935
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-301 <BEA>
A;Cross-references: EMBL:Z21814; EMBL:Z21815
A;Cross-references: EMBL:Z21814; EMBL:Z21815
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein rC:Keywords: duplication; transmembrane protein
F;7-101/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;112-204/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;209-300/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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A; Introns: 20/1; 41/3;
C; Superfamily: ADP, ATP
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                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:282059; p
A;Experimental source: clone T27E9
                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-300 <WIL>
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Best Local S
Matches 225
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Best Local Similarity
Matches 203; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMMQSGRKGT
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                                                AALWRGNLANVIRYFPTQAMNFAFKDTYKAIFLEGLDKKKDFWKFFAGNLASGGAAGATS
                                                                 LSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGATS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVMYKNTLDCWVKIGKQEGSGAFFKGAFSNVLRGTGGALVLVFYDEVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LCFVYPLDFARTRLGADVGPGAGEREFNGLLDCLKKTVKSDGIIGLYRGFNVSVQGIIIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVRIPKEQEV
                                                                                                             FLIDLASGGTAAAVSKTAVAPIERVKLLLQVQDASKAIAVDKRYKGIMDVLIRVPKEQGV 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAAYFGCFDTAKGMLPDPKNTSIFVSWAIAQVVTTASGIISYPFDTVRRRMMMQSWPCKS
 1 Similarity
225; Conserv
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                                                                                                                                                                                                                                                                                                                                                clone
                                                                                                                                                                                                                                                               carrier protein;
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78.1%;
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PIDN:CAB04874.1;
                                                                                                                                                                                              Score 1032;
Pred. No. 7
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Pred. No. 4.7e-96;
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.7e-84;
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hypothetical protein T01B11.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te: C;Accession: T25850 R;Geisel, C.; Stellyes, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein K01H12.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #teC;Accession: T23207
A; Molecule type: DNA
A; Residues: 1-313 <GEI>
A; Cross-references: EMB
                                                                    submitted to the EMBL Data Library, Decemb
A;Description: The sequence of C. elegans
A;Reference number: Z20099
A;Accession: T25850
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A; Introns: 4/1; 191/2
C; Superfamily: ADP, ATP
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Best Local
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                                                                                                                                                                                                                                                                                                                                                           TDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY 297
                                                                                                                                                                                                                                                                                                                                                                                                                         RAAYEGIYDTAKGML-PDPKNTHIVISWMIAQTVTAVAGLTSYPEDTVRRRMMMQSGRKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGIIIY
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                                                                                                                                                                                                                                                                                                                       -DVLYKNTLDCAVKIIKNEGMSAMFKGALSNVFRGTGGALVLAIYDEIQKF
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ce: clone K01H12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #sequence_revision 15-Oct-1999 #text_change
EMBL:U80931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                carrier protein; ADP, ATP
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70.8%;
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PIDN:AAB38001.1; GSPDB:GN00022; CESP:T01B11.4
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Pred. No. 1.5e
28; Mismatches
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                                                                                                                               December 1996
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                                                                                                             cosmid T01B11
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A; Experimental source: C; Genetics:
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C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
F;9-103/Domain: ADP,ATP carrier protein repeat homology <ACR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid W02D3
A;Reference number: 218308
A;Accession: T15206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
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A; Introns: 4/1; 191/2
C; Superfamily: ADP, ATP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein W02D3.6 - Caenorhabditis elegans C; Species: Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: CESP:W02D3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-300 <LET>
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      RAAYFGIYDTAKGML-PDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMMQSGRKG 246
                                                                LCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGIIIY 187
                                                                                                                                             LSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGATS 127
                                                                                                                                                                                                     FLVDLASGGTAAAISKTAVAPIERVKLLLQVSDVSETVTADKKYKGIMDVLARVPKEQGY 71
                                                                                                                                                                                                                       FAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVRIPKEQEV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Weinstock, L.; Rifkin, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -DVLYKNTLDCAVKIIKNEGMSAMFKGALSNVFRGTGGALVLAIYDEIQKF 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAAYFGIYDTAKGML-PDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMMQSGRKG 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVRIPKEQEV 67
                                                                                                                         AAFWRGNLANVLRYFPTQALNFAFKDTYKKMFQEGIDKNKEFWKFFAGNLASGGAAGATS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAAYFGMFDTAKMVFTADGKKLNFFAAWAIAQVVTVGSGILSYPWDTVRRRMMQSGRK-
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                                            LCFVYPLDFVRTRLGADVGK-GVDREFQGLTDCFVKIVKSDGPIGLYRGFFVSVQGIIIY 190
                                                                                                                                                                                                                                                                                  195;
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                                                                                                                                                                                                                                                                                  32;
                                                                                                                                                                                                                                                                                                  Score 986; DB 2;
Pred. No. 9.1e-80;
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Pred. No. 1
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A;Cross-references: EMBL:x83551; NID:g623334; PIDN:CAA58541.1; PID:g623335 C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat home C;Keywords: duplication; transmembrane protein
                                                                                                                                                                                                                   C;Species: Plasmodium falciparum
C;Date: 07-May-1995 #sequence_revision
C;Accession: S68993; S51132
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                                                            A; Molecule type: mRNA
A; Residues: 1-301 <HAT>
                                                                                                  A; Status: preliminary
                                                                                                                   A; Accession: S68993
                                                                                                                                       A; Reference number: $68993;
                                                                                                                                         Eur. J. Biochem. 228, 86-91, 1995
A; Title: Molecular characterisation of the
A; Reference number: S68993; MUID:95188918
                                                                                                                                                                                                 R; Hatin, I.; Jaureguiberry, G.
                                                                                                                                                                                                                                                                              N; Alternate names: ADP/ATP transporter
                                                                                                                                                                                                                                                                                                  ADP, ATP carrier protein - malaria parasite
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R;Hilgarth, C.; Sauer, N.; Tanner, W.
J. Biol. Chem. 266, 24044-24047, 1991
A;Title: Glucose increases the expression
A;Reference number: A41677; MUID:92084708
A;Recession: A41677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:M76669; NID:g516596; PIDN:AAA33027.1; PID:g516597 C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat hc C;Keywords: duplication; honddimer; mitochondrion; transmembrane protein E;38-134/Domain: ADP,ATP carrier protein repeat homology <ACP1> E;144-235/Domain: ADP,ATP carrier protein repeat homology <ACP2> F;241-329/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-339 <HIL>
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A; Molecule type: mRNA
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C;Accession: A41677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Species: Chlorella kessleri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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277 ---GGERQYNGTIDCWRKVAQQEGMKAFFKGAWSNVLRGAGGAFVLVLYDEIKKF
                                                                                                                                   184 IIIYRAAYFGIYDTAKGML-PDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMMQS
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                           GRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY 297
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01-Sep-1995

#text\_change 09-Jun-2000

(Plasmodium falciparum)

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| No. | Score  | Query<br>Match | Query<br>Match Length DB |    | ID       | Description        |
|-----|--------|----------------|--------------------------|----|----------|--------------------|
| 1   | 1547   | 100.0          | 298                      | 21 | AAY71032 | Human adenine nucl |
| ນ   | 1547   | 100.0          |                          | 22 | AAU01199 | Human adenine nucl |
| w   | 1454   | 94.0           |                          | 21 | AAY71033 | Human adenine nucl |
| 4   | 1454   | 94.0           |                          | 22 | AAM39641 | Human polypeptide  |
| 5   | 1454   | 94.0           |                          | 22 | AAU01200 | Human adenine nucl |
| 0   | 1454   | 94.0           |                          | 22 | AAM41427 | Human polypeptide  |
| 7   | 1411   | 91.2           |                          | 19 | AAW61169 | Antl protein. Mus  |
| œ   | 1391.5 | 89.9           |                          | 21 | AAY71031 | Human adenine nucl |
| 9   | 1391.5 | 89.9           |                          | 22 | AAU01198 | Human adenine nucl |
| 10  | 747.5  | 48.3           |                          | 21 | AAG36577 | Arabidopsis thalia |
| 11  | 747.5  | 48.3           |                          | 21 | AAG37261 | Arabidopsis thalia |

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|   | 228                | 263      | 263      | 312      | 249                | 249      | 291                | 291      | 306      | 306      | 291      | 291      | 368      | 350      | υ<br>33<br>33 | 330      | 330      | 386      | 381                | 363      | 346      | 1027     | 1009     | 992      | 381      | 381      | 381      | 381      | 363      | 363      | 363      | 363      | 346    | 346                |  |
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|   | AAG28189           | AAG16976 | AAG12918 | AAG28188 | AAG20660           | AAG39400 | AAG16975           | AAG12917 | AAG16974 | AAG12916 | AAG20659 | AAG39399 | AAG06855 | AAG06856 | AAG06857      | AAG20658 | AAG39398 | AAM00106 | AAG17729           | AAG17730 | AAG17731 | AAG38670 | AAG38671 | AAG38672 | AAG38458 | AAG37262 | AAG37259 | AAG36575 | AAG38459 | AAG37263 | AAG37260 | AAG36576 | 3846   | AAG37264           |  |
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AAY71032 RESULT AAY71032; AAY71032 standard; Protein; 29-AUG-2000 (first entry) \_ 298 A

ALIGNMENTS

Human adenine nucleotide translocator ANT2.

Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoprosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nootropic; antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia; diabetes; Lober's hereditary optic neuropathy; sohizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; 03-NOV-1998; 08-SEP-1999; myoclonic epilepsy red ragged fibre syndrome. 03-NOV-1999; 11-MAY-2000 WO200026370-A2 Homo sapiens 98US-0185904. 99US-0393441. 99WO-US25883.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, Leber's hereditary optic neuropathy, schizophrenia, mitochondrial encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is an adenine nucleotide translocator ANT2 from human brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anderson
Ghosh SS;
               mitochondrial permea
mitochondrial core c
Alzheimer's disease;
              Human: adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin; mitochondrial permeability transition pore component; cell surviva mitochondrial core component; mitochondrial related disorder; canc Alzheimer's disease; diabetes mellitus; hyperproliferative disorde
                                                                                                  Human adenine nucleotide translocator-2 (ANT-2)
                                                                                                                                     07-SEP-2001
                                                                                                                                                                                                      AAU01199 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  constructs. ANY is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 45; Page 172-173; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant construct encoding adenine nucleotide translocator polypeptide, useful e.g. in screening for potential therapeutic agents against mitochondrial disease \,\cdot\,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or ANT fusion
                                                                                                                                                                                                      Protein;
                                                                                                                                   entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     method to produce adenine nucleotide translocator fusion proteins using recombinant expression
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                                                                                                                                                                                                        298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1547;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                       Wiley SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
l.le-154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                  protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                               cell survival;
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                 disorder
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                                 cancer;
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IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG

Query Match Best Local S Matches 298

al Similarity 298; Conser

100.0%; Score 1547; DB 22; ilarity 100.0%; Pred. No. 1.1e-154; Conservative 0; Mismatches 0;

Length 298;

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298 298  $\verb|vqgiii|| yraayfgiydtakgmlpdpknthiviswmiaqtvtavagltsypfdtvrrrmmm|$ VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISMMIAQTVTAVAGLTSYPFDTVRRRMM gaagatslcfvypldfartrlaadvgkagaerefrglgdclvkiyksdgikglyggfnvs

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expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MPT and/or cell survival. These agents are useful for the prevention or treatment of diseases associated with altered mitochondrial function or dysfunctional cell survival, such as Alzheimer's disease, diabetes
Sequence
                                                                                              mellitus, Parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke,
                                                                                                                                                                                                                                                                                                                                                                   polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. green fluorescent protein (GFD) or a FLASH sequence). The novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    with other mitochondrial core components e.g. cyclophilins regulate MPT. The present invention relates to a novel nucl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transition (MTP) pore components responsible for mediating to of ADP across the mitochondrial inner membrane. ANT proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
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                                                                    hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression construct comprising a promoter operably linked to
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(ANT-2) protein. ANT proteins are mitochondrial permeability
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to energy transfer molecule
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G, Davis RE;
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                                                             disorders e.g. cancer,
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                                                                                                                                                                                                                                                                                                                                                                      The patent discloses a method to produce adenine nucleotide translocator (ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psorlasis, diabetes, dystonia, cleber's hereditary optic neuropathy, schizophrenia, mitochondrial diabetes and deafness (MIDD), and myoclonic disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
                                                                                           Query Match
Best Local S
Matches 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nootropic; antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant construct encoding adenine nucleotide translocator polypeptide, useful e.g. in screening for potential therapeutic agents against mitochondrial disease \,
                                                                                                                                                                                                                                                                                                              disorders, mitochondrial diabetes and deafness (MIDD), are epilepsy red ragged fibre syndrome. The present sequence adenine nucleotide translocator ANT3 from human brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-NOV-1998;
08-SEP-1999;
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                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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                                MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
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                                                                                                                         Similarity
Page 173-174; 175pp; English.
                                                                                                                                                                                                                                                      298
                                                                                               Conservative
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                                                                                                                            94.0%;
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                                                                                           Score 1454; DB 2
Pred. No. 7e-145;
3; Mismatches
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                                                                                                                                                       Length
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                                                                                           Indels
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25-APR-2000;
09-JUL-2000;
                   The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                         Tang
Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; nervotathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
  system,
                                                                                                                                                                                                            Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                        Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-)
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CA,
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DB; AAI58797.
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such as peripheral nervous injuries, peripheral neuropathy and
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Wang Z,
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Wehrman T,
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Velicelebi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, chemotactic/chemoskhetic activity, haemostatic and thrombolytic activity, cancer diagnosis and thrapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and assays for receptor activity, arthritis and inflammation, leukaemias and
                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                          03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin;
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DB; AAS05903.
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                                                                                                                                                        Clevenger W,
G, Davis RE;
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Pred. No. 7e-145;
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                                                                                                                                                                                 SE, Andreyev AY,
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                                                                                                                                                                                                                                                                                                                        (e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MPT and/or cell survival. These agents are useful for the prevention or treatment of diseases associated with altered mitochondrial function or dysfunctional cell survival, such as Alzhemer's disease, diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transition (MTP) pore components responsible for mediating to of ADP across the mitochondrial inner membrane. ANT proteins with other mitochondrial core components e.g. cyclophilins to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule -
                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                   mellitus, Parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke, hyperproliferative disorders e.g. cancer, and deafness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
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                                                          mtegaisfakdflaggiaaaisktavapiervklllqvqhaskqiaadkqykgivdcivr
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protein. ANT proteins are mitochondrial permeability
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Pred. No. 7e-145;
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                                                                         peripheral nervous system; neuropathy; central nervous system; Q
Alzheimer's; Parkinson's disease; Huntington's disease; haemosta
amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
chemokinetic; thrombolytic; drug screening; arthritis; inflammat
                                                                                                                                                         Human; nootropic;
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                                                                                                                                                                                             Human polypeptide SEQ ID NO 6358.
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                                                           leukaemia
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                                                                                                                                 immunosuppressant; cytostatic; gene therapy; cancer;
s system; neuropathy; central nervous system; CNS;
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New nucleic acid expression

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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
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19-OCT-2000;
29-NOV-2000;
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te: The sequence data
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qsgrkgadimytgtvdcwrkifrdeggkaffkgawsnvlrgmggafvlvlydelkk
                     QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKK 296
                                         IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
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          Similarity
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Zhou P,
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                                                                  The patent discloses a method to produce adenine nucleotide translocator (ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine dlytri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, leber's hereditary optic neuropathy, schizophrenia, mitochondrial conceptable procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the proc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 44; Page 172; 175pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant construct encoding adenine nucleotide translocator polypeptide, useful e.g. in screening for potential therapeutiagainst mitochondrial disease \,
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                                         and myoclonic
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                                                                                                                                                                                                                                                                                                          mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
                                                           New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule
                                        Disclosure; Fig
                                                                                                                N-PSDB; AAS05901.
                                                                                                                           WPI; 2001-291054/30.
                                                                                                                                               Murphy AN, C
Velicelebi G,
                                                                                                                                                                                                     03-NOV-1999;
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                                                                                                                                                                                                                                                                  WO200132876-A2
                                                                                                                                                                                                                                                                                                                                          Human; adenine nucleotide translocator-1; ANT-1;
                                                                                                                                                                                                                                                                                                                                                                 Human adenine
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263; Conserv
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G, Davis R
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                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                     99US-0434354
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                                       2; 186pp; English.
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                                                                                                                                                          Wiley SE,
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Pred. No. 2.76
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nent; cell surviva
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The present sequence represents human adenine nucleotide translocator-1 (ANT-1) protein. ANT proteins are mitochondrial permeability transition (MTP) pore components responsible for mediating transport

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RESULT 10
ÅAG36577
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Best Local Similarity 88.6%;
Matches 263; Conservative 1
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MPT and/or cell survival. These agents are useful for the prevention or treatment of diseases associated with altered mitochondrial function or dysfunctional cell survival, such as Alzheimer's disease, diabetes mellitus, Parkinson's disease, Huntington's disease, Schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke, hyperproliferative disorders e.g. cancer, and deafness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
                                                                                                                                                                                                      Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                              AAG36577 standard; Protein; 346
                                                                                              25-FEB-2000;
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                                                                                              2000EP-0301439
99US-0121825.
99US-0123180.
99US-0123548.
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99US-0126264.
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; Pred. No. 2.7e-138;
17; Mismatches 16;
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Best Local Similarity 53.9%;
Matches 166; Conservative
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13-OCT-1999;
13-OCT-1999;
Arabidopsis thaliana
           Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence.
                                         Arabidopsis
                                                                      AAG37261;
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                                                                                   standard;
                                        thaliana protein fragment SEQ ID NO: 45788
                                                       (first
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990S-0159294

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990S-0161361

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990S-0161920

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                                                                                    Protein;
                                                        entry)
                                                                                                                                                                                                                                                                                        38;
                                                                                    346
                                                                                                                                                                                                                                                                                       Score 747.5; DB 21; Pred. No. 2.3e-70; 8; Mismatches 77;
                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                      346;
                                                                                                                                                                                                                                                                                         27;
                    pathway;
promoter;
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RESULT 12
AAG37264
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Search completed: February 13, 2002, 09:33:12 Job time: 109 sec

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Q$219m xen xesculu
Q$2prh1 rana rugosa
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Q$2prh4 rana rugosa
Q$2prh5 lucilia cup
Q$1336 rana sylvat
Q$1346 rana sylvat
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Q$14093 drosophila
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Q$5129 halocynthia
Q$5126 drosophila
Q$5126 drosophila
Q$5126 halocynthia
Q$102 aeanorhabdi
P$1410 caenorhabdi
P$1410 caenorhabdi
Q$547470 dictyosteli
Q$17407 caenorhabdi
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| 45                |                   |                    |                    | 41                 |                    |                    |        | 37                 | 36                 | 35     | 34     | ω<br>ω             | 32                 | 31                 | 30                 | 29     | 28                 | 27     | 26     | 25     | 24                | 23                | 22                | 21     | 20                |
|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------|--------|--------|-------------------|-------------------|-------------------|--------|-------------------|
| 441.5             | 500.5             | 520.5              | 653.5              | 681.5              | 688.5              | 728.5              | 731    | 731.5              | 734                | 743    | 743    | 744                | 747                | 750.5              | 753                | 756.5  | 759                | 760    | 764    | 778.5  | 827               | 943               | 944               | 946.5  | 973.5             |
| 28.6              | 32.4              | 33.7               | 42.4               | 44.2               | 44.6               | 47.2               | 47.4   | 47.4               | 47.6               |        | 48.2   | 48.2               | 48.4               | 48.6               | 48.8               | 49.0   |                    | 49.3   |        |        | 53.6              | 61.1              | 61.2              | 61.3   | 63.1              |
| 158               | 162               | 327                | 262                | 298                | 330                | 305                | 317    | 305                | 331                | 386    | 379    | 388                | 306                | 385                | . 307              | 306    | 303                | 307    | 326    | 305    | 170               | 301               | 301               | 307    | 318               |
| u                 | ഗ                 | 10                 | 10                 | ហ                  | 10                 | w                  | 5      | w                  | 10                 | 10     | 10     | 10                 | w                  | 10                 | σ                  | Ų      | w                  | σ      | ა      | ω      | 6                 | 5                 | Ç                 | 80     | IJ                |
| 076467            | Q26130            | Q9LF44             | Q9AVT6             | Q21809             | Q9FM86             | Q9P875             | Q9N647 | Q9P876             | Q41628             | P93767 | 049447 | 049875             | P78754             | Q9FY52             | Q26697             | Q18683 | 074260             | 076286 | P91270 | Q9P8M1 | Q9xs69            | Q26006            | Q25692            | Q9XM22 | Q9вJ36            |
| 076467 heterodera | Q26130 plasmodium | Q9lf44 arabidopsis | Q9avt6 picea abies | Q21809 caenorhabdi | Q9fm86 arabidopsis | Q9p875 pichia jadi |        | Q9p876 pichia jadi | Q41628 triticum tu |        |        | O49875 lupinus alb | P78754 schizosacch | Q9fy52 arabidopsis | Q26697 trypanosoma |        | 074260 candida par | 9      | _      |        | Q9xs69 sus scrofa | Q26006 plasmodium | Q25692 plasmodium |        | Q9bj36 toxoplasma |

## ALIGNMENTS

| Qy<br>Db  | Оу  | Qu<br>Be  | S & C C C C C C R R R R R R R R R R R R R  | RESULT<br>O46373 |
|---|---|---|--|------------------|
| 61 IPKEQGVLSFWRGNLANVIRYEPTQALNEAEKDKYKQIELGGVDKHTQFWRYEAGNLASG 120<br> | 1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60<br> -:-  -  -  -  -  -  -  -  -  -  -  -  - | 92.2%; Score 1422; DB 6; Length 298;<br>Best Local Similarity 88.9%; Pred. No. 6.9e-122;<br>Matches 265; Conservative 20; Mismatches 13; Indels 0; Gaps | O46373; O46373; O46373; O46373; O46373; O1-JUN-1998 (TrEMBLrel. 06, Created) O1-JUN-1998 (TrEMBLrel. 06, Last sequence update) O1-JUN-2001 (TrEMBLrel. 17, Last annotation update) O1-JUN-2001 (TrEMBLrel. 17, Last annotation update) ADP/ATP TRANSLOCASE. Oryctolagus cuniculus (Rabbit). Eukaryota: Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi: Bukaryota: Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi: Nammalia: Eutheria; Lagomorpha: Leporidae; Oryctolagus. NCBL_TaxID-9986; [1] SEQUENCE FROM N.A. TISSUE-SKELETAL MUSCLE; Yamaguchi N., Kasai M.; SEQUENCE FROM N.A. TISSUE-SKELETAL MUSCLE; Yamaguchi N., Kasai M.; SUBUE-SKELETAL MUSCLE; Yamaguchi N., Kasai M.; SUBUE-SKELETAL MUSCLE; Yamaguchi N., Kasai M.; INSUE-SKELETAL MUSCLE; Yamaguchi N., Kasai M.; INSUE-SKELETAL MUSCLE; Yamaguchi N., Kasai M.; SUBUE-SKELETAL MUSCLE; Yamaguchi N., Kasai M.; INSUE-SKELETAL MUSCLE; Yamaguchi N., |                  |

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InterPro; IPR002067; Mit_carrier.
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-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDR
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Inner membrane; Mitochondrion; Transmembrane; Transport.
SEQUENCE 298 AA; 32940 MW; 91B740133751877F CRC64;
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                                                       QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
                                                                                                                                                                VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM 240
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2001 (TrEMBLrel. 17, Las
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90.3%; Pred. No. 8.6e-122;
tive 14; Mismatches 15;
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-!- SIMILARITY: TO THE MITOCHONDRIAL CAMPAGE (BY SIMILARITY).

EMBL; AY4510; CAA52616.1; -.

EMBL; AF240002; AAF64470.1; -.

EMBL; BC003791; AAH03791.1; -.

MGD: MGI:1353495; S1c25a4.

InterPro; IPR001993; Mitoch_carrier.

InterPro; IPR002067; Mit_carrier.
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01-NOV-1996 (TrembLrel. 01, Last sequence update)
01-JUN-2001 (TrembLrel. 17, Last annotation update)
ADENINE NUCLEOTIDE CARRIER (ADENINE NUCLEOTIDE TRANSLOCASE 1) (SIMILAR TO SOLUTE CARRIER FAMILY 25 (MITOCHONDRIAL CARRIER, ADENINE NUCLEOTIDE TRANSLOCATOR), MEMBER 4).
SLC25A4 OR MANCI OR ANTI.
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Pfam; pF0013; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
SEQUENCE 298 AA; 32904 MW; 3A849FEAB0981462 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Levy S.E., Chen Y.-S., Graham B.H., "Expression and sequence analysis of translocase 1 and 2 genes."; submitted (MAR-2000) to the EMBL/Gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laplace C. Submitted
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Q62164;
01-NOV-1996 (TrEMBLrel.
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STRAIN-BALB/C; TISSUE-MUSCLE;
Laplace C., Costet P.;
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Levy S.E.,
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NTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
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Sciurognathi; Muridae;
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1.6e-121;
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Q1-MAY-2000
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Q9PRH2;
Q1-MAY-2000
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01-JUN-2001
  ADP/ATr in...(Frog).
Rana rugosa (Frog).
Rukaryota; Metazoa; Chordata;
Eukaryota; Matrachia; Anura; N
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Rana rugosa (Frog).
Eukaryota; Metazoa; Chordata;
Eukaryota; Metazoa; (Amphibia; Batrachia; NCBI_TaxID=8410;
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       Neobatrachia;
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Pred.
              Craniata;
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Ranidae; Rana
       Euteleostomi;
Ranidae; Rana
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Best Local
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                                                                                                                                                                                  O9YIC4 PRELIMINARY;
O9YIC4;
O1-MAY-1999 (TrEMBLrel. 1
O1-MAY-1999 (TrEMBLrel. 1
O1-JUN-2001 (TrEMBLrel. 1
ADP/ATP TRANSLOCASE.
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDILINE-99083429; PubMed=9866197;

Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh

Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh

"The origin and differentiation of the heteromorphic s

Z, W, X, and Y in the frog Rana rugosa, inferred from
a sex-linked gene, ADP/ATP translocase.";

Mol. Biol. Evol. 15:1612-1619(1998).

-i- SUBGELJULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. No
INNER MEMBRANE (BY SIMILARITY).

-i- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
MEDLINE=99083429; PubMed=9866197;
                                                                                                                                               Eukaryota; Metazoa; Amphibia; Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00153; mito_carr; 3.
PFINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MITOCOUPLING.
PROSITE; PS00215; MITOCH_CARRIER;
Inner membrane; Mitochondrion; Tra
SEQUENCE 298 AA; 33082 MW; B0E
                                                                                                                                     NCBI_TaxID=8410;
                                                                                                                                                                         Rana rugosa (Frog).
                                                                                                                                                                                                                                                                                                          241
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                                                                                                                                                          Chordata;
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88.3%;
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Neobatrachia;
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Last annotation update)
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a; Ranoidea;
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Ranidae; Rana
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Q91336;
Q1-NOV-1996
Q1-MAY-1999
Q1-JUN-2001
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InterPro; IPR002067; Mit_carrier.
InterPro; IPR002067; Mit_uncoupling.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MTUNCOUPLING.
PROSITE; PS00215; MITOCH_CARRIER; 3.
Inner membrane; Mitochondrion; Repeat; Transmemb SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00
     INNER MEMBRANE (BY SIMILARITY).

-!- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.

EMBL; U44832; AAA97882.2; -.

InterPro; IPR001993; Mitoch_carrier.

InterPro; IPR002067; Mit_carrier.

Pfam; PF00153; Mito_carr; 3.

PRINTS; PR00926; MITOCARRIER.

PROSITE; PS00215; MITOCARRIER; 3.

Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.

SEQUENCE 317 AA; 35005 MW; 5F66B7ED8D5CEB72 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-97399141; PubMed-9256066; Cai Q. Greenway S.C., Storey K.B.; Cai G. Greenway S.C., Storey K.B.; Cai G. Greenway S.C. storey K.B.; Differential regulation of the mitochondrial in wood frogs under freezing stress."; Biochim. Biophys. Acta 1353:69-78(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Amphibia; Batrachia; Anura; Ne NCBI_TaxID=45438;
                                                                                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Rana sylvatica (wood frog).
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                                                                                                                                                                                                                                                                                                                                                 REVISIONS
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nitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 01, Created)
(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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87.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a; Craniata; Vertebrata;
Neobatrachia; Ranoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1402; DB 13;
Pred. No. 4.7e-120;
1; Mismatches 15;
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Ranidae; Rana
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Best Local S
Matches 236
                                                                                                                                                       Matches
                                                                                                                                                                                Query Match
                                                                                                                                                                    Best
                                                                                                                                                                                                                                          INNER MEMBRANE (BY SIMILARITY).
-!- SIMILARITY: TO THE MITOCHONDRIAL CARMEL, AF218587, AAF3322.1; --
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002057; Mit_carrier.
PF00153; Mito_carr; 3.
PRINTS; PR00926; MITOCARRIER: 3.
PROSITE: PS00215; MITOCH_CARRIER: 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9NHW5;
Q9NHW5;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2001 (TremBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                Chen Z., Fair J.A., Batterham P.;
"A cDNA clone encoding the ADP/ATP translocase of Lucilia cuprina.
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP/ATP TRANSLOCASE.
Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Destroidaa; Calliphoridae; Lucilia.
                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SS
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9NHW5
                                                                                                                                                                                                                       inner membrane; Mitochondrion;
sequence 300 AA; 33036 MW;
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                                                VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIFVSWMIAQSVTAVAGFGSYPFDTVRRRMMM
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TSLCFVYPLDFARTRLAADTGKGG
                        TSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGII
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236; Conserv
                                                                                                                                                                    Similarity
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Fair J.A., Batterham P.;
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Pred. No. 6
                                                                                                                                                                    Score 1235.5; DB 5 Pred. No. 7.7e-105;
-QREFTGLGNCLAKIFKSDGLVGLYRGFGVSVQGII
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Best Local :
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-I - SIMILARITY: TO THE MITOCHONDRIAL CA
EMBL; AF025798; AAB87883.1; -

FlyBase; FBgn0073292; Dpse\sesB.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; Mitoch_carrier.
Pfam; PF00153; Mitoch_carrier.
PROSITE; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER. 3.
  044094
044094;
01-JUN-1998
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SEQUENCE
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Genetica 0:0-0(1997).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila pseudoobscura (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7237;
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01-JUN-1998
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01-JUN-2001
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NON_TER 288 288
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17, Last annotation
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      Created)
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Pred. No. 1.8e-100;
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SEQUENCE
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-!- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
EMBL; AF025799; AABB7884.1; -.
F1yBase; FB9n0073237; Dsub\sesB.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; Mito_carr; 3.
PRINTS; PR00926; MITOCARRIER; 3.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                         Halocynthia roretzi (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata;
Stolidobranchia; Pyuridae; Halocynthia.
NCBI_TaxID=7729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zeng L.-W., Comeron J.M., Chen B., Genetica 0:0-0(1997).
-!- SUBCELLULAR LOCATION: INTEGRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila subobscura (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tra
Pterygota; Neoptera; Endopterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SESB.
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                                   SEQUENCE FROM N
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                                                                                                                                                                                SEQUENCE FROM N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPPDTVRRRMMMQSGR 244
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A Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Sutton G.G., Wortman J.R., Yandell M.D., Champe M., Pfeiffer B.D.,
A Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
A Ballew R.M., Basu A., Baxenhalle J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Botshakov S.,
Berkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
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Best Local
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O62526;
O1-AUG-1998 (TrEMBLrel. O7, Created)
O1-AUG-1998 (TrEMBLrel. O7, Last seque
O1-JUN-2001 (TrEMBLrel. 17, Last annot
ANT2 PROTEIN
ANT2 OR CG1683.
Drosophila melanogaster (Fruit fly).
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Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
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InterPro; IPR002067; Mit_Garrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
Inner membrane; Mitochondrion; RepeaseQUENCE 304 AA; 33306 MW; 51FD0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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nes 226; Conser
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SIMILARITY: TO THE MITOCHONDRIAL
L; D83069; BAA11765.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAGATGLCFVYPLDFARTRLAADIG-SGGSRQFTGLGNCLATIVKKDGPRGLYQGFVVS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Growth Differ. 36:39-48(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPKEQGFFSLWRGNLANVIRYFPTQALNFAFKDTYKKIFLAGVDKRKQFWRYFHGNLASG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QSGRNKEDRMYKGTVDCWGKIYKNEGGKAFFKGALSNVIRGTGGALVLVLYDELKKLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IQGIIVYRAAYFGTYDTVKGMLPDPQNTPIIVSWAIAQVVTTGAGIISYPFDTVRRRMMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76
75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
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Last annotation update)
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Pred. No. 1.9e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat; Transmemb
51FD0D7D6B654880
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a; Brachycera; Musc
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         Center A., Chandra I.,
..B., Davies P.,
Dew I., Dietz S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5:
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                                                                                                                                                                                                                                                                                                                  G.L.G.,
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RESULT Q9H0C2

DT DT AC

Q9H0C2 Q9H0C2; 01-MAR-2001 01-MAR-2001 01-JUN-2001

PRELIMINARY;
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16, 16, 17,

Last Last

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RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Douck J.,
RA Harris N.L. Harvey D.; Heinand T.J., Hernandez J.R., Duck M.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Menkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Menkulov G., Mishina N.V., Mobarry C., Morris J., McPherson D.L.,
RA Menkulov G., Mishina N.V., Murphy L., Muzny D.M., Nelson D.L.,
RA Menkulov G., Mishina N.V., Nixon K., Musskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nuxskern D.R., Pacleb J.M.,
RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spher E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Schence 287:2185-2195(2000).
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Best Local S
Matches 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER; UNKNOWN 2.
PROSTITE; PS00215; MITOCH_CARRIER; UNKNOWN 2.
SEQUENCE 307 AA; 33744 MW; 3D6B3DFD82061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhang Y.Q., Davis A.W., Root
Submitted (MAY-1998) to the
EMBL; AE003484; AAF47956.1;
EMBL; Y10618; CAA71629.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glas Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-OREGON-R;
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InterPro; IPR002067; Mit_carrier.
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                                                                                 196
                                                                                                                        187
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                   ADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK
                                                                                                                                                                                                                                                                         VLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGAT
SEMVYKNTAHCWLVIAKQEGIGAFFKGALSNIIRGTGGALVLALYDEMKK
                                                                                 YRAAYFGFYDTCRDFLPNPKSTPFYVSWAIAQVVTTVAGIASYPFDTVRRRMMMQSGLKK
                                                                                                       YRAAYFGYYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMMQSGRKG
                                                                                                                                                                   SLCFYYPLDFARTRLAADVGKGG-NREFNGLIDCLMKVIKSDGPIGLYRGFIVSVQGIVI
                                                                                                                                                                                         SLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIII
                                                                                                                                                                                                                                                   FSSFWRGNLANVIRYFPTQALNFAFKDVYKSVFLGGVDKHKQFWRHFAGNLASGGAAGAT
                                                                                                                                                                                                                                                                                                                            SFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPKEQG
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K.J., Evangelis
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                                                                                                                                                                                                                                                                                                                                                                                                                                    73.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roote J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.C., Ferraz C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                              Score 1137.5; DB Pred. No. 7.2e-96; 6; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3D6B3DFD82061C0C CRC64;
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Smith H.O.,
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Best Local S
Matches 211
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MEDLINE-94150718; PubMed-7906398;
Milson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton
                                                                                                  Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                              Q21103;
01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                    Q21103
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Mammalia; Eutheria;
                                                       Submitted
                                                                                                                                       KO1H12.2 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                              Mcmurray
                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein; Inner membrane; Mitochondrion; Transmembrane.
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                                                                                         NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                           211;
                                                                                                                                                                                                                                                                 QGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAG
                                                                                                                                                                                                                               --AKRQYKGTLDCFVKIYQHEGISSFFRGAFSNVLRGTGGALVLVLYDKIKE 306
                                                                                                                                                                                                                                         KGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK
                                                                                                                                                                                                                                                                                                     ATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGI 184
                                                                                                                                                                                                                                                                                                                                         QGFFSFWRGNLANVIRYFPTQALNFAFKDKYKQLFMSGVNKEKQFWRWFLANLASGGAAG
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                                                      (DEC-1995)
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Primates;
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72.3%;
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Last sequence update)
Last annotation updat
                                                      EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1119; DB 4;
Pred. No. 3.7e-94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             9ACE26062CCC9675 CRC64;
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                                                                                                           Rhabditida; Rhabditoidea
                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                                 43;
                                                      databases
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        Coulson
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        Query Match
Best Local S
Matches 207
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Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
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-:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
-:- SIMILARITY: TO THE MITOCHONDRIAL CARRIER
EMBL; Z68218; CAA92472.1; -.
                                                                                                                                                                                                                          STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                      Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans
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InterPro; IPR002067; Mit_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
Inner membrane; Mitochondrion; Repeat; Transmembrane; YS0215; MITOCHOndrion; Repeat; Transmembrane; YS0215; MITOCHOndrion; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Transmembrane; YS0215; MITOCHONDRIO; Repeat; Tran
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                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAAYEGMEDTAKMVETADGKKLNEFAAWAIAQVVTVGSGIISYPWDTVRRRMMMQSGRK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLIDLASGGTAAAVSKTAVAPIERVKLLLQVQDASLTIAADKRYKGIVDVLVRVPKEQGY
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                                                                                                                                                                                                                                                                                                                                                                      Nematoda; Chromadorea; rinae; Caenorhabditis.
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70.9%;
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Geisel C., Stellyes L.;
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